

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2003, 15:30:30 ; Search time 124 Seconds
(without alignments)
2694.573 Million cell updates/sec

Title: US-09-494-297-2

Perfect score: 3945
Sequence: 1 MKRFRPNKLTNTQRYLS.....IAGISLGWGTIRIRKHD 757

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QEMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-USER=US09494297 -CGN=1_1_45 -ETRNAL=13082003_122947_28128 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfillseq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	182	4.6	2187	4	US-09-107-532A-864
2	178	4.5	2694	3	US-08-867-941-2
3	178	4.5	2694	2	US-09-074-658-2
4	178	4.5	7650	3	US-08-867-941-1
5	178	4.5	7650	2	US-09-074-658-1
6	176	4.5	2718	3	US-09-074-658-69
7	161	4.1	4249	4	US-09-071-035-403
8	161	4.1	4359	4	US-09-071-035-401
9	152	3.9	5547	4	US-08-851-567B-48
10	152	3.9	7551	4	US-08-851-567B-46
11	150	3.8	3531	2	US-08-714-402-1
12	150	3.8	3698	4	US-09-327-536-1

13	149	3.8	4612	2	US-08-447-031A-8	Sequence 8, Appli
14	149	3.8	6168	4	US-09-071-035-457	Sequence 457, App
15	149	3.8	6168	4	US-09-071-035-461	Sequence 461, App
16	149	3.8	6168	4	US-09-071-035-465	Sequence 465, App
17	148	3.8	3827	2	US-08-447-031A-1	Sequence 1, Appli
18	147	3.7	15016	4	US-09-601-198-60	Sequence 60, Appli
19	145.5	3.7	2672	1	US-08-703-947-1	Sequence 1, Appli
20	142	3.6	2793	4	US-09-134-001C-2477	Sequence 2477, Ap
21	139	3.5	3695	4	US-09-071-035-419	Sequence 419, App
22	139	3.5	3840	4	US-09-071-035-417	Sequence 417, App
23	139	3.5	7101	1	US-08-480-604A-9	Sequence 9, Appli
24	139	3.5	7101	2	US-08-405-496A-9	Sequence 9, Appli
25	139	3.5	7101	3	US-08-915-136-9	Sequence 9, Appli
26	139	3.5	7101	4	US-08-957-310-9	Sequence 9, Appli
27	139	3.5	7101	4	US-10-011-366-9	Sequence 9, Appli
28	138	3.5	2682	2	US-08-867-941-7	Sequence 7, Appli
29	138	3.5	2682	3	US-09-074-658-7	Sequence 7, Appli
30	138	3.5	7641	2	US-08-867-941-6	Sequence 6, Appli
31	138	3.5	7641	3	US-09-074-658-6	Sequence 6, Appli
32	137.5	3.5	37948	3	US-09-251-645-11	Sequence 11, Appli
33	135.5	3.4	4565	3	US-08-776-265-1	Sequence 1, Appli
34	135.5	3.4	20986	4	US-08-961-527-54	Sequence 54, Appli
35	134	3.4	3057	4	US-09-601-198-55	Sequence 55, Appli
36	133.5	3.4	1878	4	US-09-697-064-1	Sequence 1, Appli
37	133	3.4	3288	4	US-09-107-532A-201	Sequence 201, App
38	132	3.3	2037	3	US-08-913-942-14	Sequence 14, Appli
39	132	3.3	2079	4	US-09-268-347-25	Sequence 25, Appli
40	132	3.3	580073	4	US-08-545-528D-1	Sequence 1, Appli
41	131.5	3.3	3894	4	US-09-107-532A-898	Sequence 898, App
42	131	3.3	1983	4	US-09-107-532A-9061	Sequence 3061, Ap
43	131	3.3	4376	1	US-08-119-125A-1	Sequence 1, Appli
44	131	3.3	6744	1	US-08-119-125A-2	Sequence 1, Appli
45	130.5	3.3	2570	2	US-09-056-075-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-107-532A-864
Sequence 864, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525
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 QY 671 oGluGlyTyrSerTyrIleu-----ValLysGluThrAspSerGluGlyTyrLysVa 688
 Db 1923 AGAAGAGATACCAAGCTTAAGAAAGACCGCAGTACTATAGTTATACAGAGATGGGTCAAT 1982
 QY 688 lLysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGlyIleThrSerAs 708
 Db 1983 TCAGTGTGATGACAGAT-----CATGAATCTGTCTGTCCACGAGAGCCAAAACAA 2036
 QY 708 pGlu--ThrLeuAlaPheGluAsnAsn--LysGluProValAlaProThrGlyValAs 726
 Db 2037 CCAGATTCTTTAGACATCAGCAATCAGCAAAAGTACCATTAACCTGAACGGGAGCAAT 2096
 QY 726 pGlnLysIleAsnGlyTyrIleuAlaLeuIleValIleAlaGlyIleSerLeuGlyIleTr 746
 Db 2097 TGCGCGTTTAGAATCTAT-----CTAGTAGGAGATGATGTTGTGCGTTTCTATTG 2150
 QY 746 P 746
 Db 2151 G 2151
 RESULT 2
 US-08-867-941-2
 : Sequence 2, Application US/08867941
 : Patent No. 5977337
 : GENERAL INFORMATION:
 : APPLICANT: Loosmore, Sheena M
 : APPLICANT: Du, Run-Pan
 : APPLICANT: Wang, Qiljun
 : APPLICANT: Yang, Yan-Ping
 : APPLICANT: Klein, Michel H
 : TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
 : NUMBER OF SEQUENCES: 67
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Sim & McBurney
 : STREET: 6th Floor, 330 University Avenue
 : CITY: Toronto
 : STATE: Ontario
 : COUNTRY: Canada
 : ZIP: M5G 1R7
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/867,941
 : FILING DATE: 03-JUN-1997
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Stewart, Michael I
 : REGISTRATION NUMBER: 24,973
 : REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (416) 595-1155
 : TELEFAX: (416) 595-1163
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2694 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single

: TOPOLOGY: linear
 : US-08-867-941-2
 Alignment Scores:
 Pred. No.: 1.28e-08 Length: 2694
 Score: 178.00 Matches: 171
 Percent Similarity: 31.48% Conservative: 118
 Best Local Similarity: 18.63% Mismatches: 305
 Query Match: 4.51% Indels: 324
 Gaps: 42
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 Db 235 ACAACGTGACCAAAATGGGATACACCAACCACTGACACAA----- 273
 QY 24 LysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
 Db 274 GCACAAAGACCGCGCTGCCGACAGGTTTGTGTGATG----- 312
 QY 44 MetValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsn 63
 Db 313 -----GGTAAATTCGTGTATACAGCCCAAAAAT---GAC 345
 QY 64 ProAspSerSerSerGlu-----TyrArgTrpTyrGly-----TyrGluSerTyrVal 79
 Db 346 CCAGATTATACCAATGATTTAGTACAGCAGTGGCAAGCAATATATATGTTGTTGAT 405
 QY 80 ArgGlyHisPro----- 83
 Db 406 GCCCATGCCCAAGATGGCATGGCACAGCTAAAAACTTGCTGACCCCATCAGCCCAAT 465
 QY 84 -----TyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
 Db 466 GACATCAAAACCTGTATTTAAACAAATCCCTGATGTGCTGATTTGATTAAGACAGT 525
 QY 99 GluLysSerArgSerTyrGlnValIleTyrCysPheAsnLeuLysValAlaPheProLeuGly 118
 Db 526 GAACGCCACCGT---TTTGACCCCAAAAGCTAAACCATTAAGTGTATGTTATGGC 582
 QY 119 SerAspSerValLysLys-----TrpTyrLysHisAspGlyIleSerThrLys 136
 Db 583 AACTTAACAAACACCTCTAAACAAACACTTACATCATCATCAGCAAGCTGATATAG 642
 QY 137 PheGluAspTyrAlaMetSerPro-----ArgIleThr 147
 Db 643 AAAAATTAACAAGCTGTGACCCCTATGAAATATCCGTTTGGGTATCTGAACCTACAA 702
 QY 148 GlyAspGluLeuAsnGlnLys----- 154
 Db 703 GGAAGCACTGTGACCAAAAAAATGCCGATCTCCAAATGACAAAGACCGCATTCACAA 762
 QY 155 ---LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly 173
 Db 763 CCCATGCCCATTTTCTTATCAGCGA-----GAAACGCCAGAGACGACCTGCCAGT 816
 QY 174 LeuGluProLeuAsn----- 178
 Db 817 GCTGTAAATTTAACTACACAGCAACTGCTGTACTAAGTATGATGCAAAAAGCGCCT 876
 QY 179 AlaIleArgValThrGlnGluAlaValIleTrpTyrTyrSerAspAsnAlaProIleSerAsn 198
 Db 877 GCACCTTCAGCATGATGATGATGGGGCTGTATTCATGATCCAGTGGCAAAATCCAT 936
 QY 199 ProAspGluSerPheLysArgGluSerLysSerLeuValSerThrSerGlnLeuSer 218
 Db 937 -----GAGGCGCATGTGTCAGTGGCGCCCATTTAT 969
 QY 219 Leu----- 219
 Db 970 CTAAGCGCTTCAATATAGCAGCAGCGCTGCACACTTATACAGTGTATTTGACACAAAC 1029

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QY 220 ---MetarglnalaLeuLysGlnLeuIleaspProAsnLeuAlaThrLysMetProLys 238
Db 1030 TCATTAACAAGCAGCGTCTATTATGACATCCCAACGACCAACTGCCAAGCAGCA 1089
QY 239 GlnValProAspSphPhe-----GlnLeuSerIlePheGluSer 251
Db 1090 TACATGATAAAGCAATTTGACACTACCAAAAAAGTCATGAAACCGATGCTATCAAAATT 1149
QY 252 GlnAspLys-----GlnAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGly 269
Db 1150 GATGCCAAATCAACGCAACCGCTTCGTCGACGCCCAATCTTGGTAAATGAGAAC 1209
QY 270 Leu-----ValProThrLysProProThrProGlyAspPro 281
Db 1210 ACAGAAACGCGACCTTTTATCAAGAGCTGTCTCCAAAAAGCAATCCCAATACCA 1269
QY 282 PrometProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGly 301
Db 1270 -----AACCTAAT----- 1278
QY 302 AspTyrSerLysLeuGlnGlyAlaThrLeuGlnLeuThrGlnAspAsnValAsnSer 321
Db 1279 -----TCAGACACGCTAGAGAGCGGTTTATGAGTCGCGCCATGAGCTG----- 1326
QY 322 PheGlnAlaArgValPheSerSerAsnAsp-----IleGlyGluArg 335
Db 1327 -----GCGGGTAATTTTATCCAAATGACACAGCACTTATGTCGCTTGGTGTAA 1380
QY 336 IleGlnLeuSerAspGlyThrTyrThrLeuThrGlnLeuAsnSerProAlaGlyTyrSer 355
Db 1381 CGAGACAAAACACAAACCTGTCGCCACAAAACGCTGATTTTATGTCGAGCGCTTGA 1440
QY 356 IleAlaGluProIleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGly 375
Db 1441 -----AAACCTGACACAGCTTTGTGATGAATGAACGATGGCAGAAATATTACAGC 1494
QY 376 LysGlnIleGlnAsnProAsnLysGluIleValGlu-----ProTyrSerVal 391
Db 1495 AAAAAGCTTAATGATCGGTGATGAGAAATGATGATGATGATGATGATGATGATGAT 1554
QY 392 GlnAlaLysAsnAspPhe-----GlnGluPheSerValLeuThr 405
Db 1555 GAACGCTATGATGAATTTCTCTGGGGCGAAAAAGCAAAATTCACCAAAAAAGTCAGC 1614
QY 406 GlnAsn-----TyrAlaLysPheTyrTyrAlaLys 415
Db 1615 AGCAGACCCCAAGCCGTCGACGCTTATTTGGGCAACATGATTAATTTTATTTT 1668
QY 416 AsnLysAsnGlySerSerGlnValTyrCysPheAsnAlaLysLeuLysSerProPro 435
Db 1669 -----AATGGCAACTATTATGACATCAGCCAGCAGAGTGTGATTAATTTGGCCCTGCC 1722
QY 436 AspSerGlnAspGlyLysThrMetThrProAspPheThrThrGlyVal----- 453
Db 1723 GATGCTGTCAAGCCCAACCAATCATTAAGAAAAAATACCTTAATGCCACATTAATAG 1782
QY 453 ----- 453
Db 1783 GACACCAAGTTACCGCATCGTGTACAAGAACCAAGATAATAAGCTTATACCGCC 1842
QY 454 -----LysTyrThrHisIleAla-----GlyArgAspLeuPhe----- 464
Db 1843 ATTCGTGCCAAAAGCATCATGACATAGTTTGGGAGAGCGCTGTATATGATGCCAAC 1902
QY 465 -----LysTyrThrValLysProArgAspThrAspThrProAspThrPheLeu 479
Db 1903 CAAACCCCAACACGCAAGTATTTTGTGCAAGCGGATGAGGAGATACACACACGCTG 1962
QY 480 LysHisIleLysLysValIle----- 486
Db 1963 CCAAGCAGGTAAATTCACCTACAAAGGCTTTGGCAGAGCTATCTATCCAAAAAAG 2022
QY 487 GlnLysGlyTyrArgGlnLysGlyGlnAlaIleGluTyrSerGly----- 501

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Db 2023 GACAAAGCTTATGCAATATATGAGAAACCATCAAGAAAAAGCCATCAAGATTATCTG 2082
QY 502 LeuThrGlnThrGlnLeuArgAlaIleThrGlnLeuAlaIleTyrTyrPheThr----- 519
Db 2083 TTAACCAAGAC-----TTACCCACGAGAA 2106
QY 520 -----AspSerAlaGlnLeuAspLysAspLysLeuLysAspTyrThrHisGlyPhe 535
Db 2107 GATGATGACATGATTTGACCGCATGTCATGATGATCAAGATGATGATGATGATGATGAT 2166
QY 536 GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp 555
Db 2167 GATGATTTG-----ATTGCATCTGATGATTCACAAAGAT 2199
QY 556 SerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGln 575
Db 2200 GATGACGACAGATGCGCATGACAGATTCAGATGATTTG-----GTCATGTCGACATGAC 2253
QY 576 SerLeuIleGlyThrGlnThrPheProGluAspLeuValAspIleIleArgMetGluAsp 595
Db 2254 GCGCGCGCAGCAAGATGATTCATGACAGTAAT-----ATTCGCCCTGAATTT 2301
QY 596 LysLysGluValIleProVal-----ThrHisAsnLeuThrLeu----- 608
Db 2302 GAAACAAATACTTGGCCATTAATGAGCCTACTACATGAAAAACCTTTGCCCTAGATGGT 2361
QY 609 -----ArgLysThrValThrGlyLeuAlaGly 617
Db 2362 AAAAATTAACCTAAGTTGATGTCGATTTTGACACCAACGCTTAAGTAAATTAAC 2421
QY 618 AspArgThrLysAspPheHisPheGlnIleGlnLeuLysAsnAsnLysGlnLeuLeu 637
Db 2422 GATGACAGAGATGATATCGCTTGAATATC-----AAAAATGCCAAATGATGGCACA 2475
QY 638 SerGlnThrValLysThrAspLysThrAsnLeuGlnPheLysAspGlyLysAlaThrIle 657
Db 2476 GGCTTTACCGCCCAACCGCATGTGCCAACTATCTGAGAGAACTGGGT----- 2523
QY 658 AsnLeuLysHisGlyLysLeuThrLeuGlnGlyLeuProGluLysTyrSerTyrLeu 677
Db 2524 AACACCAACAGTGGC-----GTTTCTTATACAAAC 2553
QY 678 ValLysGlnThrAspSerGlnGlyTyrLysValLysValAsnSerGlnGluValAla--- 696
Db 2554 ATCAAGATATTGATGCAAGGGCAATTTTGGCACAATAATGCGAAGGTGGCAGGG 2613
QY 697 -----AsnAlaThrValSerLysThrGly 704
Db 2614 CAGTTACAGTACGACAAAGCGCATGTCATCAATGACACCGCGCAAAAGCAGGG 2667

RESULT 3
US-09-074-658-2
; Sequence 2, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: QiuJun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074.658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2694 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-074-658-2

Alignment Scores:
Pred. No.: 1.28e-08 Length: 2694
Score: 178.00 Matches: 171
Percent Similarity: 31.48% Conservatve: 118
Best Local Similarity: 18.63% Mismatches: 305
Query Match: 4.51% Indels: 324
DB: 3 Gaps: 42

US-09-494-297-2 (1-757) x US-09-074-658-2 (1-2694)

QY 4 ThrArgpHeProAsnLysLeuAsnThrLeuAsnThrInArgValLeuSerLysAsnSer 23
   ||| ||||| ||| |||||
DB 235 ACAACTGACCCCAATGGCGATACCAACCACTGCACAAA----- 273
QY 24 LysArgpHeThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
   :::: ||| ||| ||||| |||||
DB 274 GCACAAAGACCGCCGCGTCCGACGGTTTTGTGATG----- 312
QY 44 MetValGlyAlaLysThrValPheGlyLeuValGlySerSerThrProAsnAlaIleAsn 63
   ||| :::: ||| ||||| |||||
DB 313 -----GCTAAATTCGTGATACACGCCCAAAAAT---GAC 345
QY 64 ProAspSerSerSerGlu-----TyrArgTrpTyrGly-----TyrGlySerTyrVal 79
   ||||| ||||| :::: ||| |||||
DB 346 CCAGATTATACCAATGATTAGTACAGACGTCGCAAGCAAAATTATATGTTGTTGAT 405
QY 80 ArgGlyHisPro----- 83
DB 406 GCCCATGCCCGCAGATGCGACAGTAAAACTTGCGTACGCCCATCACCCTCAAT 465
QY 84 -----TyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
   ||||| :::: ||| ||||| |||||
DB 466 GACATCAAAACCTTGTATTTTAACAAAATCCCTGCATTTGTGATTTGATTTAGACAT 525
QY 99 GlyGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLysAlaPheProLeuGly 118
   ||| ||| :::: ||| ||||| |||||
DB 536 GAACCCCAACCGT---TTTGACCCCAAAAAAGCTAAACACCATTAAGTATGTTATGTC 582
QY 119 SerAspSerSerValLysLys-----TrpTyrLysLysHisAspGlyIleSerThrLys 136
   :::: :::: ||| ||||| |||||
DB 583 AACTTAACACACCCCTCTAAACACACACTTACATCAATCATCAGACCAAGCTATATTAAG 642
QY 137 PheGluAspTyrAlaMetSerPro-----ArgIleThr 147
   :::: ||| |||||
DB 643 AAAAATAACAAGCCCTGTGACCCCTTATGAAATATCCGTTTGGTATCTTAACATACAA 702
QY 148 GlyAspGluLeuAsnGlnLys----- 154
DB 703 GGAACAGCTGTGACCAAAAAAATCCGATACCTCAATGACAAAGACCGCATTCACAA 762
QY 155 ---LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlyGly 173
   :::: ||||| ||||| ::::

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DB 763 CCCATGCCCATTTTGTTTTATCAGCA-----GAAAGCCGACGACGCGTCCACT 816
QY 174 LeuGluProLeuAsn----- 178
DB 817 GCTGTAATATTAACTACACAGCAACGCTGTACTTAAGTATGATCAAAAAAGCCCT 876
QY 179 AlaIleArgValThrGlnAlaValAlaTyrTyrTyrSerAspAsnAlaProIleSerAsn 198
   ||||| :::: ||| ||||| |||||
DB 877 GCATCTTACAGCATGATGATGAGTGGGGCTGTATCTCAAAAGCCAGTGGCAAAATCCAT 936
QY 199 ProAspGlySerPheLysArgLysGlySerGlySerAsnLeuValSerThrSerGlnLeuSer 218
   ||| :::: ||||| |||||
DB 937 -----GAGGCGCATGTGTAGTGTCCGCCCATTTAT 969
QY 219 Leu----- 219
DB 970 CTAAAGCGCTTTCATATATAGCACACAGCGCTGCCACTTATCAGTGTGATTTGACACAAAC 1029
QY 220 ---MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys 238
   :::: ||| ||||| |||||
DB 1030 TCATTAAACGAGCAAGCTGTCTTATATATGACAAATCCCAACGACCAAGTCCACAGGCACA 1089
QY 239 GlnValProAspAspPhe-----GlnLeuSerIlePheGlySer 251
   ||| |||||
DB 1090 TCATCAAAAGCCATTTTGACACTACCAAAAAAGCATGAACGATGTATCAAAAT 1149
QY 252 GlnAspLys-----GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGly 269
   :::: ||| ||||| |||||
DB 1150 GATGCCAAATCAACGCGCAACCGCTTCGCGGTACGCGCCCAAAATCTTGTGTATATGAGAAC 1209
QY 270 Leu-----ValProThrLysProProThrProThrProLysAspPro 281
   :::: ||||| |||||
DB 1210 ACAGAAACCGCACCTTTATTCAAAGAGCGTGTCTCCAAAAAGCAATCCCAATTAACCA 1269
QY 282 PrometProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGly 301
   |||||
DB 1270 -----AACCCATAT----- 1278
QY 302 AspTyrSerLysLeuGlnGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer 321
   ||| ||||| |||||
DB 1279 -----TCAGACACCGCTGAAGCGGTTTATGTGATGAGTCCGCGATGACCTG----- 1326
QY 322 PheGlnAlaArgValPheSerSerAsnAsp-----IleGlyGluArg 335
   ||| ||| ||||| |||||
DB 1327 -----GCGGTAATTTTATTCCAATGCAACGATCTTATGTGCTTGTGGGTAA 1380
QY 336 IleGluLeuSerAspGlyTyrThrTyrThrLeuThrGlnLeuAsnSerProAlaGlyTyrSer 355
   :::: ||| |||||
DB 1381 CGAGACAAACAGACAAACCTGTCGCCCAAAACGGTGTATTTAGTCCAGCTTTGAA 1440
QY 356 IleAlaGluProIleThrPheLysValGlnAlaGlyLysValTyrThrIleIleAspGly 375
   :::: ||| ||||| |||||
DB 1441 -----AAACCTAGACCGCATTTTGTGATATGAAGATGCGAGATTTATTAACACG 1494
QY 376 LysGlnIleGluAsnProAsnLysGluIleValGlu-----ProTyrSerVal 391
   ||||| :::: ||| ||||| |||||
DB 1495 AAAAAGTTAATGATGAGCGGTGAAGAAATTTGATGATATTCCTCCAGCTGAT 1554
QY 392 GlnAlaTyrAsnAspPhe-----GluGluPheSerValLeuThrThr 405
   ||| ||||| |||||
DB 1555 GAACGCTATGATGATTTCTTCTGGGCGGCAAAAAAGCAATTTACCAAAAAAGTCACG 1614
QY 406 GlnAsn-----TyrAlaLysPheTyrTyrAlaLys 415
   :::: ||| ||||| |||||
DB 1615 ACAGACACCCCAAGCGGTGCACCTATTTTGGCAACATGATAAATTTATATTT----- 1668
QY 416 AsnLysAsnGlySerSerGlnValTyrCysPheAsnAlaAspLeuLysSerProPro 435
   ||||| :::: ||| ||||| |||||
DB 1669 -----AATGCAACTTATATGATCAGACGACGATGTTGATTAATTTGCGCCCTGCC 1722
QY 436 AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluVal----- 453
   ||||| :::: |||||
DB 1723 GATGCTGTCAAGCAACCAATTCATTAAGAAAAAATACCTTAATGCCACACTAATATAG 1782

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OY	453	-----	453
Db	1783	GACAAACCAAGTACCAGCATCGTCGCTACAGAAAGCCAAAGATTAATTAAGCCCTTATACCGCC	1842
OY	454	-----LysTyrThrHisIleAla--GlyArgAspLeuPhe-----	464
Db	1843	ATTGCTGCCAAAGAGCTATACAGCATCAGTTTGGCGAGCGCTATATACAGATGCCAAC	1902
OY	465	-----LysTyrThrValIlePheProArgAspThrAspProAspThrPheLeu	479
Db	1903	CAAAACCCCAACGCGATGATTTGTGCMAAGCGGTAGCGAGATACCAGACCAACGCTG	1962
OY	480	LysHisIleIleLysValIle-----	486
Db	1963	CCCAAGCAGGTAATTCATCTTACACACGCTTTGGCGAGCCTATCTTAACCAAAAAAG	2022
OY	487	GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGly-----	501
Db	2023	GACAAAGGTTTATAGCAATATAGAAACCATCAAGAAAAAGCCATCAAGATTTACTG	2082
OY	502	LeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPheThr-----	519
Db	2083	TTAACCCGAAGAC-----TTACACCCAGAA	2106
OY	520	-----AspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe	535
Db	2107	GATGATGACGATGATTTGACCCGACATCTGATATTCACAAAGATGATGATGACAGCGCAT	2166
OY	536	GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp	555
Db	2167	GATGATTTG-----ATTGATGTGATGATTCACAAAGAT	2199
OY	556	SerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnLysTyrGln	575
Db	2200	GATACACGACATGCGCATGATGACGATTCACATGATTTG-----GGTGATGTGACATGAC	2253
OY	576	SerLeuIleGlyThrGlnThrPheIleProGlnLysPheValAspIleIleArgMetGlnAsp	595
Db	2254	GCCCGCGGACGACAAAGTGTATCATGACAGTAAAT-----ATTGCGCCGTGAATTT	2301
OY	596	LysLysGluValIleProVal-----ThrHisAsnLeuThrLeu-----	608
Db	2302	GAACAAACAAATAGTCCCATTAATAGCGCTAGTCAAAAAACCTTTGCCCTGATAGTG	2361
OY	609	-----ArgLysThrValIleThrGluLeuAlaGly	617
Db	2362	AAAAATTAAGCTAAGTTGATGCGATTTTGACACCAACACCCCTAAGCTGTAATTAAC	2421
OY	618	AspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnLeuLeu	637
Db	2422	GATGAGAGAGGTGATTCGCTGTTGATATC-----AAAAATGCCAAATATGATGGCACA	2475
OY	638	SerGlnThrValLysThrAspLysThrAsnLeuGluIlePheLysAspGlyLysAlaThrIle	657
Db	2476	GCGTTTACCGCCCAAGCGCATGTGCCAAACTATGCTGAAGAAAGGGGT-----	2523
OY	658	AsnLeuThrHisGlyGluSerLeuThrLeuGlnIleLeuProGluGlyTyrSerTyrLeu	677
Db	2524	AACAAACCAAGGTGC-----GGTTCTTATCAAC	2553
OY	678	ValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnIleValAla--	696
Db	2554	ATCAAAAGATATGATGTCAAGGGCAATTTTGGCACAATAATGGCGAAGCTTGGCAAGG	2613
OY	697	-----AsnAlaThrValSerLysThrGly	704
Db	2614	CAGTTACAGTACGACAAAGCGGATGCGATCAATGACACCGCCGAAAAAGCAGGG	2667

```

: GENERAL INFORMATION:
: APPLICANT: Loostore, Sheena M
: APPLICANT: Du, Run-Pan
: APPLICANT: Wang, QuiJun
: APPLICANT: Wang, Yan-Ping
: APPLICANT: Klein, Michel H
: TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
: NUMBER OF SEQUENCES: 67
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sim & McBurney
: STREET: 6th Floor, 330 University Avenue
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/867,941
: FILING DATE: 03-JUN-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Stewart, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-681 MIS:jd
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7650 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-867-941-1

Alignment Scores:
Pred. NO.: 7.03e-08 Length: 7650
Score: 178.00 Matches: 171
Percent Similarity: 31.48% Conservative: 118
Best Local Similarity: 18.63% Mismatches: 305
Query Match: 4.51% Indels: 324
Gaps: 42
DB:

US-09-494-297-2 (1-757) x US-08-867-941-1 (1-7650)
Oy 4 ThrAArgPheProAsnLysLeuAsnThrGlnArgValLeuSerLysAsnSer 23
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Db 375 ACAACGACGCCAATGGCATATACAAACCAACACGACACACA----- 4133
Oy 24 LysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
::: ||| ||| |||||
Db 414 GCACAAAGACGCCCGCCCTGCCGACAGGGTTTGTGTGATG----- 4522
Oy 44 MetValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsn 63
||| ::| ||| ::|
Db 453 -----GGTAAATTCGTGTATACACGCCCAAAAAAT--GAC 4855
Oy 64 ProAspSerSerSerGlu-----TyrArgTrpTyrGly-----TyrGluSerTyrVal 79
||||| |||:::| ||| ::| |||
Db 486 CCAAGATTATTAAGCATATGATTAGTACAGACAGTGGCAAGCAAAATTATATGTTGGATTGAT 5455
Oy 80 ArgGlyHisPro----- 83
|||
Db 546 GCCCATGCCCAAGATGCATCGCACAGGTAAAACTTGCGTCAGCCCATACCGCCCAT 6055
Oy 84 -----TyrTrpLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
|||:::| |||:::| |||:::|
Db 606 GACATCAAAACCGTTGATTATTTTAAACAATATCCCTCGCATTTGCTGTGATTTGCATTAGACAGT 6655

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QY	99	GIuGIysErArGSeRrYGIuValrYrYcysPheAsnLeuLysLysAlaPheProLeuGly	118
Db	666	GAAGCCACCGCT---TTTGACCCCAAAAAAGCTAAACACATTAAAGTATGGTTATG	722
QY	119	SerAspSerSerValLysLys-----TPrYrLysSHIsAspGlyLeSerThrLys	136
Db	723	AACTTAACAACACCCCTCTAAAAACACACTTACATCATCATCAGCAAGCTGATATANG	782
QY	137	PheGIuAspTYrAlaMetSerPro-----ArgIleThr	147
Db	783	AAAATATACAAGCCTGTGGACCCCTATGAAATATCCGTTTGGGTATCTGAAC	842
QY	148	GIyAspGIuLeuAsnGlnLys-----	154
Db	843	GGAAGCAGCTGACGACCAAAAAATGCCATCTCCAAATGACAAAGCCGATGCCAAA	902
QY	155	---LeuArGAlaValMetTYrAsnGlyHIsProGlnAsnAlaAsnGlyLeMetGluGly	173
Db	903	CCCATGCCCATTTTGTATTATCAGGA-----GAAAACGCCAGCAGCTGCCAGT	956
QY	174	LeuGIuProLeuAsn-----	178
Db	957	GCTGTAAATTAACTACACAGGCAACTGGCTGATCTCAATGATGATCAAAAAAGCCCT	1011
QY	179	AlaIleArGValThrGlnAlaValAlaPTrYrTYrSerAspAsnAlaProIleSerAsn	198
Db	1017	GCATTTTCAGCATGATGATGATGATGGGGGTCTATCTCAATGCCAGTGGCAATTCAT	1076
QY	199	ProAspGIuSerPheLysArgGIuSerIuSerAsnLeuValSerThrSerGlnLeu	218
Db	1077	-----GAGGCGATGTCGTGATGCGCCGCCACATTTAT	1105
QY	219	Leu-----	219
Db	1110	CTAAACGGCTTCAATATAAACACAGCCCTGCCACTTATCAGGTGATTTGACCAAAAC	1166
QY	220	---MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys	238
Db	1170	TCATTATACAGCAGCATGCTCTTATATGACATCCCAACGAAACATGCCCAAGCAAA	1222
QY	239	GlnValProAspAspPhe-----GlnLeuSerIlePheGluSer	251
Db	1230	TACATCAAAAAGCCATTTTGACACTACCAAAAAAGTCAATGAAACCGATGTATCAAAAT	1288
QY	252	GluAspLys-----GlyAspLysTYrAsnLysGlyTYrGlnAsnLeuSerGlyGly	269
Db	1290	GATGCCAAATCAACAGCGCACCGCTCTCGGTACGCCCAATCTTGTGTTATATAGAAC	1344
QY	270	Leu-----ValProThrLysProProThrProGlyAspPro	281
Db	1350	ACAGAACAACCGCACTTTATCAAAAGAGCTGTTCTCAAAAAAGCAATCCCAATTAACCA	1400
QY	282	ProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTYrAlaIleGly	301
Db	1410	-----AACCTTAAT-----	1418
QY	302	AspTYrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer	321
Db	1419	-----TCAGACACCGCTAGAGGCGGGCTTTATGTGTAGTGGGGGATGAGCTG-----	1466
QY	322	PheGlnAlaArGValPheSerSerAsnAsp-----IleGlyLysLuarG	335
Db	1467	-----GGGGTAAATTTTATTCCAATGACAAACGATCTTATGTGCTTTGGTGGTAA	1522
QY	336	IleGluLeuSerAspGlyThrTYrTYrLeuThrGluLeuAsnSerProAlaGlyTYrSer	355
Db	1521	CGAACAACAAACGACAAACCTGTGCGCCCAAAAAAGGTATTTTATGACAGGCTTTGAA	1580
QY	356	IleAlaGluProIleThrPheLysValGlnAlaGlyLysValTYrThrIleIleAspGly	375
Db	1581	-----AAACTTACACCATGTTTGTGTGATATGAAACGATTTGGCAGATTTATTAACAC	1633
QY	376	LysGlnIleGluAsnProAsnLysGluIleValGlu-----ProTYrSerVal	391

Db	1635	AAAAAGTTAAATGATGCGGTGAATGAGAAATTTGATAATGCTGATATTCTACACAGTCAT	1694
Qy	392	GLuAlaYrAsnAspPhe-----GluGluPheSerValIleuThrThr	405
Db	1695	GAACGCTGTGATGAAATTTCTTGGGGCCAAAAAAGCAGAAATTCACCAAAAAAGCTGAC	1754
Qy	406	GlnAsn-----TyrAlaLysPheTyrTyrAlaLys	415
Db	1755	AGCAGCACCCCAAGCGCGTACGACTATTGTTGGCCAAACATGATAATTTATATTTT	1808
Qy	416	AsnLysAsnGlySerSerGlnValValIlyrcysPheAsnAlaAspLeuLysSerProPro	435
Db	1809	-----AATGGCAACTATTATTAACCTATACAGCCACAGCACTGGTGAATAATTTGGCCCTTGCC	1862
Qy	436	AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThlGlyLVal-----	453
Db	1863	GATGCTGTCAAAAGCCACCAATCCATTAAAGAAAATATCCCTAATGCCACATAATTAAG	1922
Qy	453	-----	453
Db	1923	GACAAACAAATACCGCATCGTGTGTACAGAAAGCCAAAGATAATTAACCTTTATACGCC	1982
Qy	454	-----LysTyrThrHisIleAla---GlyArgAspLeuPhe-----	464
Db	1983	ATTCGTGCCAAAGACTATACACACATCAGTTTGGCGAGCGACTGTATTAACGATGCCAAC	2042
Qy	465	-----LysTyrThrValLysProArgAspThrAspProAspThrPheLeu	479
Db	2043	CAAAACCCCAACGCGAGTTATTTTGTGCAGAGCGGTAGGAGATACACGACGACGCGTG	2107
Qy	480	LysHisIleLysLysValIle-----	486
Db	2103	CCCAAGGAGGTAATTTACCTATACAGCGTCTTTGGCAGCGCTATCTTATCCAAAAAAG	2162
Qy	487	GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSergly-----	501
Db	2163	GACAAAGGTATTAGCAATAATGAAGAAACCATCAAGAAAGGCGCATCAAGATTATCTG	2222
Qy	502	LeuThrGluThrGlnLeuAlaAlaIleThrGlnLeuAlaIleTyrTyrPheThr-----	519
Db	2223	TTAAACCGAAGAC-----TTACCCCGACAA	2246
Qy	520	-----AspSerAlaGluLeuAspLysAspLysLysAspTyrHisGlyPhe	535
Db	2247	GATGATGACGATGATTTCACCGCATCTGATGTTACAGATGATGATGACATGGCGAT	2306
Qy	536	GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp	555
Db	2307	GATGATTTTG-----ATTGCATCTGATGATTACCAAGAT	2339
Qy	556	SerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGln	575
Db	2340	GATGACGCGATGGCGATGACGATGATCAATATATTG-----GCGTAGGTCGACAGATGAC	2393
Qy	576	SerLeuIleGlyThrGlnTyrHisProGluAspLeuValAspIleIleArgMetGluAsp	595
Db	2394	GCCGCGGACGAGCAAAAGTATCATGTCAGAGTAAT-----ATTGCGCCGTGAATTT	2441
Qy	596	LysLysGluAlaIleProVal-----ThrHisAsnLeuThrLeu-----	608
Db	2442	GAAGAAACAATCTTGCCCATTAATGACGCTACTGATCAAAAAACCTTTGGCCCTAGATGCT	2501
Qy	609	-----ArgLysThrValThrGlyLeuAlaGly	617
Db	2502	AAAAATAAAGCTAAGTTTGATGTGGATTTTGACACCAACACCCCTTAACCTTAATTAAC	2561
Qy	618	AspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeu	637
Db	2562	GATGAGAGAGGTGATATGCTGTTGATATC-----AAAAATGCCAAATATGATGGCCACA	2615
Qy	638	SerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle	657

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Db      2616  GGGCTTTACCCGCAAGCCGAGTGTGCCAACATATCGTGAAGAAGTGGT----- 2663
QY      658  AsnLeuLysSHSgLyGIuSerLeuThrLeuGInGlyLeuProGInGlyTyrSerTyrLeu 677
      |||  |||
Db      2664  AACACCAAGGATGCG-----GTTCTTTATACAA 2693
QY      678  ValLysGluThrAspSerGInGlyTyrLysValLysValAsnSerGInGlyValAla--- 696
      ::|||::|||  |||  |||
Db      2694  ATCAAAAGATTGATGTCAGAGGGCAATTTTTGGCACAAATGGCGAAGAGTTGGCAGGG 2753
QY      697  -----AsnAlaThrValSerLysThrGly 704
      |||  |||  |||  |||
Db      2754  CAGTTACAGTACGACAAAGCGGATGCGATCATGACACCGCCGAAAGACAGGG 2807

RESULT 5
US-09-074-658-1
: Sequence 1, Application US/09074658
: Patent No. 6184371
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M
: APPLICANT: Run-Pan Du
: APPLICANT: Quijun Wang
: APPLICANT: Yang, Yan-Ping
: APPLICANT: Klein, Michel H
: TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Slim & McBurney
: STREET: 6th Floor, 330 University Avenue
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/074,658
: FILING DATE: 08-MAY-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Stewart, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-795
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7650 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-074-658-1

Alignment Scores:
Pred. No.: 7,03e-08 Length: 7650
Score: 178.00 Matches: 171
Percent Similarity: 31.48% Conservative: 118
Best Local Similarity: 18.63% Mismatches: 305
Query Match: 4.51% Indels: 324
DB: 3 Gaps: 42
US-09-494-297-2 (1-757) x US-09-074-658-1 (1-7650)
QY      4  ThrATgPheProAsnLysLeuAsnThrLeuAsnThrgInArgValLeuSerLysAsnSer 23
      |||  |||  |||  |||
Db      375  ACAAGTCAGCAAAATGGCGATACACCACTGACACACA----- 413
QY      24  LysATgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
      ::|  |||  |||  |||

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US-09-074-658-69

Alignment Scores:

Pred. No.:	2,12e-08	Length:	2718
Score:	176.00	Matches:	164
Percent Similarity:	33.42%	Conservative:	102
Best Local Similarity:	20.60%	Mismatches:	264
Query Match:	4.46%	Indels:	266
		Gaps:	40

US-09-494-297-2 (1-757) x US-09-074-658-69 (1-2718)

QY 84 TyrTrpLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSer 103
 Db 493 TATTTGATAAATTCCTCCAAATATCCGATCTG-----CACCTAGAAAAACAGCGAG-- 543
 QY 104 TyrGlnValTyrCysPheAsnLeuLysGlyAla-----PheProLeuGly 118
 Db 544 -----CATGTGTTGATGCTAAATAAGCAATATCAATAATATATGTTATGT 594
 QY 119 SerAspSerValLysLys-----TrpTyrLysHisAspGlyLe 133
 Db 595 GCATTTGCATCACCCTGCCAAAACCACTACATGATATATCAACAAGAACAAACATC 654
 QY 134 SerThrLys-----PheGluAspTyrAla-----MetSerProArg 145
 Db 655 AAAAACAAAAACCAGCGCATGATATCAAAACATCTGTTTGGCTATATGAGACTAGA 714
 QY 146 IleThr-----GlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
 Db 715 GAGCTGACCTAAATATAAAAGTGCGACAGACCCAGAGCGACAAAGACCGTGCATATTT 774
 QY 160 TyrAsnGly-----HisProGlnAsnAlaAsnGlyIleMetGluGlyLeu 174
 Db 775 TTCACCCACACTACTTATTTTATTCATGATGAGAGATCCAGACCACTCTGCCA----- 828
 QY 175 GluProLeuAsnAlaIleArgValThrGlnGluAlaValTyrTyrSerAspAsnAla 194
 Db 829 -----AAGCGGGTAAATTTGACTATGAGGCGCAATTTGTTGATCTGACGAGATGC 879
 QY 195 Pro-----IleSerAsnProAspGlu-----SerPhe 203
 Db 880 AAAAACGCCCATTTTATAGATATAAACAGAGATATAAGCTAGGCACTTATTTAACTCAAC 939
 QY 204 LysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu----- 219
 Db 940 AGAAATTCAAATGAAGCGCATTTGGTGTGAGTGACACACATTTATCTAAACAGCTTTAA 999
 QY 220 -----MetArgGlnAla 223
 Db 1000 TATAAACACACCCCGCCACTTATAGCGTGTGACTTTGATCAATAATACCTTAAAGCGCAA 1059
 QY 224 LeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp 243
 Db 1060 TTGTCTTATTATGACACCCCAACCAACAGCAAGCGGATGGCGTTATATCAAGAGTCAAG 1119
 QY 244 Phe-----GlnLeuSerIlePheGluSerGlnAspLys----- 254
 Db 1120 TTGTATATACGACAAAAAGTCAATGAAGCGGATGTCTATGAGATGAGCGCAAGATTAA 1179
 QY 255 GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyLeu----- 270
 Db 1180 GGCAACCGCTTACTGTGCACAGCCCAATCTTATGATTGATATAACCAATACCGCACT 1239
 QY 271 -----ValProThrLysProProThrProGlyAspProPheMetProProAsn 286
 Db 1240 TTGTGTTAAAGAGCTGTTCTCAAAAAAACCAATCCCAACACCA-----GACCCCAAC 1293
 QY 287 GlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306
 Db 1294 -----TCAGATACG 1302
 QY 307 LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVal 326

Db 1303 CTAGAAAGCGCGTTTATGCTGAGTCCGGCGATGACCTG-----GCGGGTAAA 1350
 QY 327 PheSerSerAsnAspIle-----GlyGluArgGlyLeuLeuSer 339
 Db 1351 TTTTATCAATGACCAACGCAACCTTTTGTGTCTTTGGTGGTACCAACAGCAACACACC 1410
 QY 340 AspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluPro 359
 Db 1411 GAACCTGTCCGCACAAAAACGGTGTATTAGT--ACAGATTTGAA-----AAACC 1461
 QY 360 IleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGlyLys----- 376
 Db 1462 AGCACCGCTTTGTTGGCAATGGAAGATTTGTAGCATTTATTCGCGTAAAGTTAAAT 1521
 QY 377 ---GlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsn 395
 Db 1522 GATCAAGTCAATATCAATCAATTTGAAGATGAAGAACTGTCCCTGTCTAATAAAGATTTAT 1581
 QY 396 AspPhe-----GluGluPheSerValLeuThrThr 405
 Db 1582 GAATATATATTATGACGACGCCAACCAATTCACCAAAAAATMAAGCCACGCTCCAA 1641
 QY 406 GlnAsnTyrAla-----LysPheTyrTyr----- 413
 Db 1642 AAAAACCCCTCTATTGTTGGTCAGCATGATGAATTTATTTATGTTAATGTTACTATTATGAC 1701
 QY 414 -----AlaLys-----AsnLysAsnGlySerSerGlnValTyrCysPheAsnAla 429
 Db 1702 TTTATCAGCCAAAGACAAAGCAACCTTTGGTGTGTCTCCCAACATATCCAGCACCAATTAAGAGT 1761
 QY 430 AspLeuLysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPheThr 449
 Db 1762 ATTTTGGCTAATATACCAAGATGCC-----AAAGTAAAGCAACATATAAAGTT 1809
 QY 450 Thr----- 450
 Db 1810 ACCAAATCGCTGTACAAACAGCCAAAGATTAAGCCGTATCCGCCATTATGCCAAAGC 1869
 QY 451 -----GlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
 Db 1870 TATGACCACATCAGTTTGGTGAAGTATTTGATTAATGATATACAAAGGCAACCAACACGC 1929
 QY 465 LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLys----- 480
 Db 1930 AGTATTTTGTGCAAGCGGTCAAGCGGATGTCAAGTACTAGCTGCCACAGTGAAGTAA 1989
 QY 481 -----HisIleLysLysValIleGluLysGlyTyrArg 491
 Db 1990 TTCACCTATATGCTGTTTGGGCAAGCGTACTACCCAGAAAGCAAAAGCTTTATAGC 2049
 QY 492 GlyLysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnThrGlnLeuArgAlaIleThr 511
 Db 2050 AAAGATGAGATACCATCAACAAAGCAAAAGGCTTAAAGAT----- 2088
 QY 512 GlnLeuAlaIleTyrTyrPheThr----- 519
 Db 2089 -----TATATATTGACCAAAAGACTTTATCCACAAAGATGACATGACATGAC 2136
 QY 520 AspSerAlaGluLeuAspLysLysLeuLysAsp---TyrHisGlyPheGlyAspMet 538
 Db 2137 GATAGTTTGAAGCCCATCTGATGATTCACAAAGATGAATATACATGCGCGATGATTTGG 2196
 QY 539 AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrGlnIleAspSerAsnPro 558
 Db 2197 -----ATTGCACTGTGATGATTCACAAAGATGATGACACAA 2229
 QY 559 ProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIle 578
 Db 2230 GATGGGATGACATTCAGATGATTTG-----GGTAGTGTGCACATGATGACGGCGCA 2283
 QY 579 GlyThrGlnThrProGluAspLeuValAspIleIleArgMetLysAspLysGlu 598
 Db 579 GlyThrGlnThrProGluAspLeuValAspIleIleArgMetLysAspLysGlu 598

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Db 2284 GCGAAAGTGTATCATGCAGTAAT-----ATTGCGCCCTGAATTTGAAAACAA 2331
Qy 599 ValIeProVal-----ThrHisAsnLeuThrLeu----- 608
Db 2332 TACTTGCCCATTAATGACCTACTCATGATAAAAAACCTTTGCCCTAGATGTAATAAATAG 2391
Qy 609 -----ArgLysThrValThrGlyLeuAlaGlyAspArgThr 620
Db 2392 GCTAAGTTTGATGTAACCTTTGACACACACAGCCCTACTGCTAATTAACGATCAGAGA 2451
Qy 621 LysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuSerGlnThr 640
Db 2452 GGTATATCGCTCTTGATATC-----AAAAATGCAAAATTTGATGCGACAGATTTTACC 2505
Qy 641 ValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLys 660
Db 2506 GCCAAAGCCGATGTGCCAACTATCGTGAAAGAGTGGT-----AACCAACCA 2553
Qy 661 HisGluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGlu 680
Db 2554 GGTGGC-----GGTTCTTATACACATCAAGAT 2583
Qy 681 ThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluAla 696
Db 2584 ATTGATGTTAAGGGCAATTTTGGCACAAATGCGCAAGAGTTGGCA 2631

RESULT 7
US-09-071-035-403
: Sequence 403, Application US/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071.035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brookes
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 403:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4249 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-09-071-035-403

Alignment Scores:
Pred. No.: 1.72e-06 Length: 4249
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326

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Query Match: 4.08% Indels: 166
DB: 4 Gaps: 40
US-09-494-297-2 (1-757) x US-09-071-035-403 (1-4249)
Qy 39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGlySer----- 56
Db 1451 TCATTAACTACACCGTAAATGTCCTTAATAAGCATTCATTAATGATCCGATCAATAT 1510
Qy 57 ---SerThrProAsnAlaIleAsnProAspSerSerGlyTyrArgTyrGlyTyr 75
Db 1511 ATTGAACCAATTAGTGTGTTAAATCC---TTGAATGCTGAAACCTGTTGGGTAATAT 1567
Qy 76 GluSerTyrValArgGlyHisProTyrTyrLysGlnPheAlaValAlaHisAspLeuArg 95
Db 1568 GATCAA-----AATGTCCTATTCATCAAGA 1594
Qy 96 -----ValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113
Db 1595 ACAACTGCTCAGTTATGGAAGCAAGAACGATTCAAATTTGAAATTAAGTA 1654
Qy 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrPyrLysLys 129
Db 1655 AAGCATCCTAATTATCTTCAATTACAGACTCAAAAGAAATTTATTTTATTAACAG--- 1711
Qy 130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
Db 1712 -----TTAGAACG-----GATTATACAGTAAAGCCACGTCAGATGGTTCA 1753
Qy 150 GluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlnHisProGlnAsnAlaAsnGly 169
Db 1754 GTTATTAGTTCACATACGCCCAATTAACCAAGCAATTCCAATTTGTTTAATAT 1813
Qy 170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
Db 1814 GTGCGCAGTACTTGGCCAAAGATAAAGTATCCAGTCGATACGATCCCATTAACAATG 1873
Qy 185 GluAlaValIleTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
Db 1874 AGTCGTGAAGGTTTAACTCCAGTTGATACGACAGTAATCTACT-----AATAGTA 1924
Qy 205 ArgLysSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
Db 1925 CGTGTTCTGAACGACACACTTCAAGTAAGTAATAATCCTTGTCATAGCAGCAAT 1984
Qy 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
Db 1985 GATTCTTTGACTCACTAAGCGTCGTCACAAATAATCCAGCTGGCGCC-----GATGTT 2038
Qy 245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
Db 2039 CTTTGTGACATTTATGATGATGTTCAAC-----GATCAGTAGATTCATTTATCCACAA 2092
Qy 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheMetPro 284
Db 2093 TACTGGAGCGCGGTCATACTTTGATTAACCAATGACGCCAAGCCGCGATATGCCA 2152
Qy 285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296
Db 2153 ACGATTACTTTTGACGAAATAACCAATGATTACAGCTTTGATTTGGAAAAACCAACAA 2212
Qy 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGlnGlyAlaThrLeuGln 313
Db 2213 GGTTRACATTTAT---GAGTATTAATAAACGCCCAATGCGTGGATCGCAACTCTTTAT 2269
Qy 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
Db 2270 ATAACAGGACAGCAAGAAAGAACCAACATCAATATAATAGAGCTGCTGCTTCT 2329
Qy 328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
Db 2330 GTTCAAAAT-----GAAGCGTTAGACATTTTGAATGTCAGACA----- 2365

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QY 348 LeuanserProalaglytyrSerllealaglProlethrPhelyValgluagly 367
Db 2366 -----CAAGCGCGAATCCAACTTAAATAATGTAACAAACG 2404
QY 368 LysVallythr---lleleaspglylys-----glntleglueanproasnlyglu 384
Db 2405 ACAGTAAACAAACAAATAATGTAATTAATAACACATGCTGTGAATAATCCAAACATGAA 2464
QY 385 lleValgluProtyrSerValgluAlaTyraasnphleglugluPheserlleuThr 404
Db 2465 TTAAACCAAAAGGACACCAACCAATGCTCAATGATTTGATTTATACCGTG----- 2518
QY 405 ThrGlaasnTyralalyspethyrytyralalysasnlysaenglyserSerGlnVal 424
Db 2519 -----AAAGCGCGCGCAAGATGCT 2539
QY 425 TyrcysPheasnalaaspleuLysSerProProaspSerGlnaspglylysthrMet 444
Db 2540 TAT-----TCATTAGACAGAGACTCAAAACGCTGCGAAAGTCAT 2578
QY 445 ThrProspheThrThrlyglu-----VallysthrHisllealaglyArg 461
Db 2579 TTAAAGACTTATACATTGACAGAAACATTACGATTAATACATACCGTCTCGCAAC 2638
QY 462 AspleuPhelystyrThrVallysProatgAspThrAspProaspThrPhelysnHis 481
Db 2639 GCTGGCCAAATCTATACAGAAACAAACATGACCTGTAACATTTGAACSCAGATGCTGCT 2698
QY 482 llelylyValle-----GluLys 488
Db 2699 AGCAAGAAAAAGTCACACACTGCGCAATCACATTGAATTCAGAAAGTGATGCGGAA 2758
QY 489 GltYrArggluLysgluAlailegluTyrseryleuThrGlnleuArg 508
Db 2759 GGTATGTTTATTAGCAACTGCCACATTTACACGATACATACGATAGAGTGAACCA 2818
QY 509 AlalalThrGlnleuAlailetyrtyrPhethrAsp-----SeralagluLeu 524
Db 2819 GCAATGCGAAGGTTCTTTGAACTAATGATTAATGATCAACGATACAGAACCGAATTT 2878
QY 525 AspleuAspleuLysAspyrHisglyPheglYasmet---AsnaSpserThrleu 543
Db 2879 ACAACAGATGAAAAAGTCAATCTCTTTGATGCCATTCAGACAGGTGATTTACTTGG 2938
QY 544 AlaValalalyslleuValgluTyraaglInasPserasnProProGlnleuThr--- 562
Db 2939 CGAGTAAAGAAATGACCGCAGCAATATTCCTGATGACAAG-----TATTGACAGGA 2992
QY 563 -----AspleuAspPhehlePro----- 569
Db 2993 AAAGCATTAAGCTGCTCAAGAGAGACAAACCACTAAATAATTCATTAACGAAACAAAT 3052
QY 570 AsnaAsnlystyrGln-----SerleuilegylthrGlntrPhisPro 584
Db 3053 GATCACAGTCGTTTACAGTCAAGATTCACAGATTATATCGCGCATTCATGCAACCA 3112
QY 585 GluAspleuValasplelleargmetgluAspleLys---GluValilleProvalThr 603
Db 3113 GAAGAG-----AACTTTGTTTCAAGCAGACAGATTAACAGAGTCAAGAGCTTCCCTCGAA 3166
QY 604 HisAsnleuThrleuArglysthrValThrGlyleuAlaglyAspArgthrLysAspPhe 623
Db 3167 -----AAATCACTGTTTCAAGTCAAGTGAATTAACAAACAGAGGCTT 3211
QY 624 HisPhegluilegluLeuLysasnlysglngluLeuLeuSerGlnthrVallysthr 643
Db 3212 TATCCATTAATTAACGTGACGAGGTAAAGAAACACACCTATGTCAGCGTCAAAACC 3271
QY 644 AspleuThrAsnleuPhelyAspGlyAlaThrleuAsnleuLysHisglu 663
Db 3272 GACCAATCTAAGTTAGGTCAAAGAT-----ACAACGATTTATGTT-----GGTAT 3319
QY 664 SerleuThrleuGlnleuProgluGlytyrSerTyrlleuVallysgluThrAspSer 683

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Db 3320 TCGTGCAA-----CCAGAA-----GATTAATTCGTTTCAGCGACAGCAAA 3361
QY 684 GluGlytyrlysthrVal-----LysValasnSerGlnleuValAlaAsnAlaThrVal 700
Db 3362 ACAGGTCACAGACGCTTCCGTTTGAATAATGATGTTTCAGGAAACAGTGAAT-----GTT 3415
QY 701 SerlysthrGlylleThrSerAspGluThrleuAlaPhegluasn 715
Db 3416 GATTAATAATGAC-----GATTATGAATTTGTCTATAATAAT 3451

RESULT 8
US-09-071-035-401
: Sequence 401, Application us/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071,035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brookes
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 401:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-09-071-035-401

Alignment Scores:
Pred. No.: 1.79e-06 Length: 4359
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326
Query Match: 4.08% Indels: 166
DB: 4 Gaps: 40

US-09-494-297-2 (1-757) x US-09-071-035-401 (1-4359)
QY 39 AlaLeuValThrserMetValgluAlaLysThrValPheglYleuValgluSer----- 56
Db 1546 TCATTAAGTACACCTGTAATTTGCTTAATAAAGCATTCATTAATGATCCGATCAATAT 1605
QY 57 ---SerThrProAsnAlaileasnProAspSerSerSerGluTyraArgthrtyrGlytyr 75
Db 1606 ATTGAAACCAATTAATGTTGTTATCTCT---TTGAATGCTGAAACCTGCTGGGTATATAT 1662
QY 76 GluSerTyraValarglyHisProtyrTyrlYsglnPheargValAlaHisAspleuArg 95

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Db 1663 GATCAA-----AATGTCCTATTCAACAGA 1689
 QY 96 -----ValAsnLeuGluClySerArgSerTyrGlnValTyrCysPheAsnLeuLys 113
 Db 1690 ACACTGCTCTCAGTTATGGGAGCAAGAAAGCAACCGATTCAAAATTTAGCAAAATTTAAAGTA 1749
 QY 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrPylrLysLys 129
 Db 1750 AAGCATCTCAATTATCTTTCATTACGAGCTACAAAAGAAATTTATTTTATTATCAAG---- 1806
 QY 130 HisAspGlyLysSerThrLysPheGluAspTyrAlaMetSerProArgLleThrGlyAsp 149
 Db 1807 -----TTAGAACG-----GATTATACAGTACGCCACGTCAGATGGTTCA 1848
 QY 150 GluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
 Db 1849 GTTATTAAAGTTCAGTACGCCAATTAACCAAGAAATTCAAATTCCAATTTGTTTAAATTTAT 1908
 QY 170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
 Db 1909 GTCCACAGATAGTTTGCACAAAAGATAAAGTATCCAGTCGATACGATACCGATACCAATG 1968
 QY 185 GluAlaValTyrPylrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
 Db 1969 ACTGCTGAAGTTTAACCTCAGTGTACGACAGTAACTACT-----AATAGTAG 2019
 QY 205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
 Db 2020 CGTGGTCTGGAACGAACTTCAAAAGTAAATAAATCAATTCCTTGTCAATGCACGCAAAAT 2079
 QY 225 LysGlnLeuLleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspHe 244
 Db 2080 GATTCTTTGACTACTAGCGTCCGTACAAAATTTCCAGCTGGCC-----GATGTT 2133
 QY 245 GlnLeuSerLlePheGluSerGlyAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264
 Db 2134 CTTTTGACATTAATGATGTTTCAAA-----GATCAGGTAGATTCATTAATTCACAA 2187
 QY 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheMetPro 284
 Db 2188 TACTGGGACCGGCTCAATCTTGTGATTAACCAATGACGCCCAACGCCCTGGATATCCA 2247
 QY 285 -----ProAsnGlnProGlnThrThrSerValLeuLle-----Arg 296
 Db 2248 ACGATTACTTTGACGAAATAATCCCAATACTTACAGCTTGATTGGAAAAACCAACAA 2307
 QY 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGlnGlyAlaThrLeuGln 313
 Db 2308 CGTTACATTAAT---GAGTATATAAAACGCCAATGCGTGTGACGTGCCAATCTTTAT 2364
 QY 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
 Db 2365 ATTAACAGGACAGCAAAACCAACCAATGCAATTAATGAAGCGCTCTCTCGCTTCT 2424
 QY 328 SerSerAsnAspLleGlyGluArgLleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
 Db 2425 GTTCAAAAT-----CAACGCTTAGCATTTTGAATGCAACA----- 2460
 QY 348 LeuAsnSerProAlaGlyTyrSerLleAlaGluProIleThrPheLysValGluAlaGly 367
 Db 2461 -----CAAGCGCGAATTCACACATTTAAAAATTCACAAAAAG 2499
 QY 368 LysValTyrThr-----IleIleAspGlyLys-----GlnIleGluAsnProAsnLysGlu 384
 Db 2500 ACAGTAACAAACAAAATAATTTGATATAAACAACATCGGTGAAAAATTCACACGATTGTA 2559
 QY 385 IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerLeuThr 404
 Db 2560 TTAAACACCAAAAGCAACCAATGCTCAATGATTGAATTCATTATTCGGG----- 2613
 QY 405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal 424
 Db 2614 -----AAGGCGCTGCCACAAAGATGCT 2634

QY 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
 Db 2635 TAT-----TATTAGAAAGACTCAAAACGGTGGCAAGTCAAT 2673
 QY 445 ThrProAspPheThrThrGlyGlu-----ValLysTyrThrHisIleAlaGlyArg 461
 Db 2674 TTAAAGACTATATCTTATGACAGAAACAAATTAGATTTGATATACATACATACGCTCTCGCAAC 2733
 QY 462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481
 Db 2734 CTTGCCAAATCTATACAGAAACAAACAAATCGACTCTGAAACATTGACACAGATGCTGCT 2793
 QY 482 IleLysLysValIle-----GluLys 488
 Db 2794 AGCAGAAAAAAGTCAACGACCTGCCCAATCAATGAAATTTCTCAGAACGTATGCGCA 2853
 QY 489 GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArg 508
 Db 2854 GGTATTTGTTTATTAGCAACCTGCCACATTTCTACGCCATACAGGTAGAGATGAAACCA 2913
 QY 509 AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu 524
 Db 2914 GCAATTCGCAAGCTTTCTTTGAACTAATGATTAATGTCACCCATACACCAACCGAATTT 2973
 QY 525 AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet-----AsnAspSerThrLeu 543
 Db 2974 ACAACAGATGAAGAAAGGTCAATATCTCTTATGATGCCATCATACAGATGATTAATCTTG 3033
 QY 544 AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProProGlnLeuThr 562
 Db 3034 CGAGTAACAAATGTACCGCAGAAATATTCGGTGAATGAAGAG-----TATTGACAGGA 3087
 QY 563 -----AspLeuAspPhePheIlePro----- 569
 Db 3088 AAGCCATTAACTGCTGTCAAAGACACCACTAAATTCATTAACGAACAAAT 3147
 QY 570 AsnAsnAsnLysTyrGln-----SerLeuIleGlyThrGlnThrPhePro 584
 Db 3148 GATCAACAGCTGTTTACAACTCAACATTCACAGATTTATGTCGACATTCATCAAGAAACCA 3207
 QY 585 GluAspLeuValAspLleIleArgMetGluAspLysLys-----GluValIleProValThr 603
 Db 3208 GAAAGG-----AACTTCTTTCACGACACAGATTAACAGCGTCAAGCTTCCTTCGAA 3261
 QY 604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspHe 623
 Db 3262 -----AAATTCACCTGTTTCAGGTCAAGTTGATTAACANCAACAGCGCTT 3306
 QY 624 HisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643
 Db 3307 TATCCAAATTATTACAGTACGACGAGGTAAAGAAACAGCTATGTGACCGTCAAAACCC 3366
 QY 644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663
 Db 3367 GACCAATCTTAAGTTAGAGTCAAGAT-----ACACGATTTATGCT-----GCTGAT 3414
 QY 664 SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683
 Db 3415 TCGTGGAAT-----CCAGAA-----GATTAATTCGTTTCACGACAGACAA 3456
 QY 684 GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700
 Db 3457 ACAGTCAGACAGCTTCCGTTGAAAAAATGATGTTCCAGGAGCAACAGTGAT-----GTT 3510
 QY 701 SerLysThrGlyTyrThrSerAspGluThrLeuAlaPheGluAsn 715
 Db 3511 GATTAATAATAGC-----GATTATGAATTTCTATAAAAT 3546

RESULT 9
 US-08-851-567B-48
 ; Sequence 48, Application US/08851567B
 ; Patent No. 6528484

GENERAL INFORMATION:

APPLICANT: Ensign, Jerald C

APPLICANT: Bowen, David J

APPLICANT: Petell, James

APPLICANT: Fatig, Raymond

APPLICANT: Schoonover, Sue

APPLICANT: French-Constant, Richard

APPLICANT: Rochelleau, Thomas A.

APPLICANT: Blackburn, Michael B.

APPLICANT: Hey, Timothy D.

APPLICANT: Melio, Donald J.

APPLICANT: Orr, Gregory L.

APPLICANT: Roberts, Jean L.

APPLICANT: Strickland, James A.

APPLICANT: Guo, Lining

APPLICANT: Cliche, Todd A.

APPLICANT: Sukhplinda, Kitiisri

TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dow Agrosciences Patent Department

STREET: 9330 Zionsville Road

CITY: Indianapolis

STATE: IN

COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,567B

FILING DATE: 05-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/063,615

FILING DATE: 18-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/395,497

FILING DATE: 28-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/007,255

FILING DATE: 06-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/608,423

FILING DATE: 28-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/705,484

FILING DATE: 28-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.93804

TELEPHONE: 608-251-5000

TELECOMMUNICATION INFORMATION:

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 5547 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-851-567B-48

Alignment Scores:

Pred. No.: 2.4e-05

Score: 152.00

Percent Similarity: 33.13%

Best Local Similarity: 18.29%

Query Match: 3.85%

DB: 4

Length: 5547

Matches: 148

Conservative: 120

Mismatches: 287

Indels: 254

Gaps: 37

US-09-494-297-2 (1-757) x US-08-851-567B-48 (1-5547)

QY 157 AlavaLmctyrnsnglyHisProGlnAsnAlaAsnGlylleMetGluGluPro 176

2386 GCACMACAAATGATATGCGGCCACAGGGCGTTTCCCTTGGTC---GGGTGATAT 2442

QY 177 LeuSnAlaIleatGValThrGlnGlu---AlaValrPrpYrYrSerAsp----- 192

2443 ATTCAATCAATGAAAGACACCGACCTATGCCAGTGGGAAAAAGCGGCGCATTTA 2502

QY 193 -----AsnAlaProIleSerAsnProAspGluSerPheValArgGluSerGlu 208

2503 ACCGCGGTTGAATTCACAAAGCCTAATATACCTATTTCGATGATCTCGC 2562

QY 209 SerAsnLeuValSerThr-----SerGlnSerIleuMetArgGlnAlaLeuLys 225

2563 AGTCCCGCATTAACCACTACTATATCCGTCAAGTCGCCAAGCAGCGGCGCATTTAA 2622

QY 226 Gln-----LeuIleAspProAsnLeuAla----- 233

2623 AGCCGTGATGACTTGATCATCTTACTTACTTATATATGAGTTTCTGCGCAATPAA 2682

QY 234 ---ThrLysMetProLysGlnValProAspAspPheGlnLeu----- 246

2683 ACCACCGGATGCGCGCAAGCCATTGCC---AGTATTCACCTGACGTCAACCGGCATTG 2739

QY 247 ---SerIlePheGluSerGluAspLysGly----- 255

2740 GAAATGTGAGAAAGAAATGCCAATTCGGGGGTATTCAGCCGCCAATTCCTTATGACTGG 2799

QY 256 AspLysTrpAsnLysGlyTrpGlnAsnLeuSerGlyLysLeuValProThrLysPro 275

2800 GACAATACATATAAGCCTACAGACACTTGCGGGCTTCTCATTAGTTACTACCCG 2859

QY 276 ProThrProGlyAspProPheMetProProAsnGlnProGlnThrThrSerValLeuIle 295

2860 GAAACATATATTTGATCCGACCATGCGTATGCGAACAACAAATGATGAGCATTACTG 2919

QY 296 ArgLysTyrAla----- 299

2920 CAATCCGTCAGCCAAACCAATTAACCGCGCATACCTCGCAAGATGCTTATGTCTTAT 2979

QY 300 IleGlyAspTrpSerLysLeuGlnGlyAlaThrLeuGlnLeuThrGlyAspAsnVal 319

2980 CTGACATCGTTTGACAAAGTGGCTAATCTTAAGTATTTAGCCATATACGATATATAT 3039

QY 320 AsnSerPheGlnAlaIleValPhe-----SerSerAsnAspIleGlyGlu--- 334

3040 AATAACGATCAAGGGCTGACCTATTATTCGAGCTCGTGAACCTGATGCGGTGATAT 3099

QY 335 -----ArgIleGluLeuSerAspGlyThrYrThrLeuThr----- 346

3100 TATTTGGCGCATGCTTCATCATCAATTAACGACGATTAATTCGGCGCTAATGCTGTG 3159

QY 347 -----GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360

3160 AGTGAATGCGATTAATGATGTGTCATTAATACCTTAATAAGCACTATCCGTCAGTG 3219

QY 361 ThrPheLysValGluAlaGlyLysValTyrThrIle---IleAspGlyLysGlnIleGlu 379

3220 ATATATATAA-----TCCGCGCTATCTCTCTGTTGGACAAAAGGAGATCACC 3270

QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluIleAlaTyrAsnAspPheGlu--- 398

3271 AAACACACAGAAATTAAGATGGCTATCAACACTGAACGCAATTAATCTTATGACATA 3330

QY 398 ----- 398

3331 AAATGGCGCATATCCGCTATGATGCGACTTGGAATACGCCAATACACTTGTATGTCAT 3390

QY 399 ---GluPheSerValLeuThrThrGlnAsn-----TyrAlaLysPhe 411

--- 411 ---

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Db 3391 AAAAAATATCCGAGCTAAAACTGGAAAAAATAGAGCCCGGAGCTCTATTGTGCCGT 3450
Oy TyrTyrAlaLysAsn-----
Db 412 TATCAAGGTGAAGATAGCTTCTGCTGATGTTTATTAACAACAAGACACTAGATAGT 416
Oy 3451 TATCAAGGTGAAGATAGCTTCTGCTGATGTTTATTAACAACAAGACACTAGATAGT 3510
Oy 417 ---LysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
Db 3511 TATAAAGCGCTCATGCAAGACTATATATCTTT---GCTGATNTGGCATCC----- 3561
Oy 436 AspSerGluAspGlyGlyLysThrThrPro-----
Db 3562 ---AAAGATATGACCCGACAGACAGACAATGTTTATCGGATAT 3603
Oy 446 -----
Db 3604 AGCTATCAACAATTGATACCAATATATGTCAAGAGTGAATACCGCTATGCAAGAT 3663
Oy 447 -----AspPheThrThrGlyGluValLysTyr 455
Db 3664 TATGAGATTCCTCTCCTCGTGAAGTAGCGCTAAAGCTATGTTGGGAGATTTATTCCTC 3723
Oy 456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
Db 3724 AGCATGTATATTAACGAGATATTCACACTATCAATTAACAAGCCGATCAAGTATTTA 3783
Oy 476 AspThrPheLeuLysHisIleLysValIleGlyLysGlyTyr-----Arg 491
Db 3784 AAAATCTATATCTCAACCAAAATTAAAGAAATTATCTTAATGATATGAAGAGACAGAGCGC 3843
Oy 492 GluLysGlyGlnAlaIleGlyLysSerGlyLeuThrGlnLeuArgAlaIleThr 511
Db 3844 AATCAATGATCATGATCAATTAATATGCAAACTAGAGTATTAATTTATGTTTATCT 3903
Oy 512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531
Db 3904 AGCTTGGGGCTCAATCCAAATTAACGTCATTAATAGCTCATGTTTACCCGCTATCA 3963
Oy 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValIle 551
Db 3964 TATAGCGGA-----ACACACGATGACTCAATCAAGGAGACTACTA----- 4005
Oy 552 TyrAlaGlnAspSerAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAsn 571
Db 4006 TTCACCGCTGACACACTTATCCA-----TCTAAGTAGAAGCTTGATTCCTGGAGCA 4059
Oy 572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTyr----- 582
Db 4060 AAAGCTTCTTAACCAACCAAAATGCGCGCATGTGATGATTAATGCTACAGACTCTG 4119
Oy 583 ---HisProGluAspLeuValAspIleLeuArgMetGluAspLysLysGluValIle--- 600
Db 4120 AATAAAGCGGATGATTAACCAATATATCTTATGACTGACAGTAAGGAGACTGCTACT 4179
Oy 601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValIleThr 613
Db 4180 GATGCTCAAGGCCAGTAGAATTAATACGCAATTTCTCCAGCAAAAGTTCAAGTATA 4239
Oy 614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626
Db 4240 CTCAAAGCGGCTGCAAGAGCAAACTTTTACCGAGATAAAGATGCTCCATTCAGCCA 4299
Oy 627 -----IleGluLeuLysAsnAsnLys 633
Db 4300 TCACCTAGCTTTGATGAATAATTAATTAATTAATGCTGAATGAGCGTCTCTGT 4359
Oy 634 GlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652
Db 4360 CTGAATTTTATTAACACTCAAGCAGATGATGATGTTTACCGCATTTGGCGAGAGAT 4419
Oy 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662
Db 4420 GCGCGCAAACTGGGTTATGAAGTTTCAGTATTCCTGTTACCTCAAGTAAAGTACCAT 4479

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Oy 663 GluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluThrAsp 682
Db 4480 AATGCCCTGACCCCTGACCACTAATGAATAATGCTGCGCAATATATG-----CAA 4527
Oy 683 SerGlnGlyTyrLysValLysValAsnSer-----GlnGluValAlaAsnAla 698
Db 4528 TGGCAATCTTAATCGAACCGGCTGAAATCTCATTTGCCCGCAGTTGTTGCCACCGCC 4587
Oy 699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718
Db 4588 ACC-----ACCGAATGATGATCAATTCGATATGGAACACTCAAGAAATTCAGGAA 4638
Oy 719 ProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIle 738
Db 4639 CCG-----CAGTTAGCAAAAGGTTTCTATGCTACGTTGCTGATTA 4677
Oy 739 AlaGlyIleSerLeuGlyIleTyrPheLys 747
Db 4678 CCTCCCTAATACCTATCAACTCATGCT 4704

RESULT 10
US-08-851-567B-46
; Sequence 46, Application US/08851567B
; Patent No. 6528484
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Faltz, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Cliche, Todd A.
APPLICANT: Sukhapinda, Kitisri
TITLE OF INVENTION: Insecticidal Protein Toxins From Phototribabus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: Dow AgroSciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296, 93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7551 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-851-567B-46

Alignment Scores:
Pred. No.: 3,97e-05 Length: 7551
Score: 152.00 Matches: 148
Percent Similarity: 33.13% Conservative: 120
Best Local Similarity: 18.29% Mismatches: 287
Query Match: 3.85% Indels: 254
DB: Gaps: 37

US-09-494-297-2 (1-757) x US-08-851-567B-46 (1-7551)
QY 157 AlaValMetYrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluPro 176
DB 2650 GCACAAACATTTGATGTCGCCCAAGGCGTTTCGGCTTGGTC--GGCTGATATAT 2706
QY 177 LeuAsnAlaIleArgValThrGlnGlu--AlaValTrpTyrTyrSerAsp----- 192
DB 2707 ATTCATTCATAGAAAGACACGACGACCTATGCCAGTGGGAAACCGGACGCGATATTA 2766
QY 193 -----AsnAlaProIleSerAsnProAspLeuSerPheLysAlrGluSerGlu 208
DB 2767 ACCGCGCGGTGATACACACAGCTAATACATTAACACCTTTCTGATGATCTCGC 2826
QY 209 SerAsnLeuValSerThr-----SerGlnLeuSerLeuMetLrGlnAlaLeuLys 225
DB 2827 AGTGGCCGATTAAGCACTACTATATTCCTGCAAGTCGCAAGCGGCGGCTATTAA 2886
QY 226 Gln-----LeuIleAspProAsnLeuAla----- 233
DB 2887 AGCCGATGACTTGTATCAATACTTACTGATTGATTAATACAGTTTCTCGCGCAATAAA 2946
QY 234 ---ThLysMetProLysGlnValProAspAspPheGlnLeu----- 246
DB 2947 ACCACCCGATCCCGAAGCAGCATGGCC--AGTATTCACTGTACGTCAACCGCGCATTG 3003
QY 247 ---SerIlePheGluSerGluAspLysGly----- 255
DB 3004 GAAATAGTGGAATAAATGCAATTCGGGGGTTATACGCCGCCAATTTCTTATGACTG 3063
QY 256 AspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyLysValProThrLysPro 275
DB 3064 GCAAAATACATTAAGGCTACACACTTGGCGGGGCTTTCATATTAGTTACTACCG 3123
QY 276 ProThrProGlyAspProPheMetProProAsnGlnProGlnThrSerValLeuIle 295
DB 3124 GAAATCATATGATCCGACCATGCTATTCGACAAACCAAAATGATGACGATATACG 3183
QY 296 ArgLysTyrAla----- 299
DB 3184 CAATCGCTGACGCAAAACCAATTAAAGCGGATACCGTCGAGATGCTTATGCTTAT 3243
QY 300 IleGlyAspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnVal 319
DB 3244 CTCACACTGGTTTAAACAAGGCTATCTTAAAGTTATTAAGCCATATCAGATATATT 3303
QY 320 AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyGlu--- 334

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DB 3304 AATACAGATCAAGGCGTACCTATTATTCGACTGAGTGAACATGATCGCGTGAATAT 3363
QY 335 -----ArgIleGluLeuSerAspGlyThrThrThrLeuThr----- 346
DB 3364 TATTCGCGCATGCTCATCACTACACTAATATTCACAGCGGTAATTCGCGCTAATGCTTG 3423
QY 347 -----GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360
DB 3424 AGTGAAATGGCATTAATGATTGTGCAATTAACCTTTAATAAAGACATTCGCTCAAGTG 3483
QY 361 ThrPheLysValGluAlaGlyLysValTyrThrIle---IleAspLysGlnIleGlu 379
DB 3484 ATATATATAA-----TCCCGCTGTATCTGCTCTGGTTGGACAAAAGAGATACCC 3534
QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaLysAsnAspPheGlu--- 398
DB 3535 AAACAGACAGAAATAGTAAGATGGCTATCAAACTGAACAGGATTAATGCTTATGAACTA 3594
QY 398 ----- 398
DB 3595 AAATGGCGCATATCCGCTATGATGGCAGCTTGGAAATACGCAATCAGCTTGTATGTCAT 3654
QY 399 ---GluPheSerValLeuThrThrGlnAsn-----TyrAlaLysPhe 411
DB 3655 AAAAATAATATCCGCTAAACCTGAAACAAAATAGACGCGCGAGCTCTATTGTGCGGCT 3714
QY 412 TyrTyrAlaLysAsn----- 416
DB 3715 TATCAAGGTGATACATCGTTGCTGATGATTTTATTAACCAACAGACACACTAGTACT 3774
QY 417 ---LysAsnGlySerSerGlnValTyrCysPheAsnAlaAspLeuLysSerProPro 435
DB 3775 TATATAAAGCGCTCATATGACAGCATATATATCTT--GCTGATATGATCATC-- 3825
QY 436 AspSerGluAspLysLysThrMetThrPro----- 446
DB 3826 -----AAAGATATGACCCGAGAACAGACAGACAGATGTTATCGGATAT 3867
QY 446 ----- 446
DB 3868 AGCTATACAAATTTATACCAATATATGTCAGAAAGTGAATACCGCTATGACAGAGAT 3927
QY 447 -----AspPheThrThrGlyGluValLysTyr 455
DB 3928 TATGAGATTCCTCTCTCGAATAGTACCGTAAAGACTATGTTGGGAGATATATTAAC 3987
QY 456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
DB 3988 AGCATGTATATTAACGAGATATATCCAACTATCAATTAACAAACCGCATCAAGTATTA 4047
QY 476 AspThrPheLeuLysHisIleLysValIleGluLysGlyTyr-----Arg 491
DB 4048 AAATATATATATCTACCAACAAATTAAGATATTTCAATATGATATTAAGACAGAAAGCC 4107
QY 492 GluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuAlaAlaThr 511
DB 4108 AATCAATGCAATGTGATGAATAAATATGCAAACTAGTGATTAATTTATTTAT 4167
QY 512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531
DB 4168 AGCTTGCGGCTCAATCAATAATACCTGTAATAATAACTCATGTTTACCCCGCTATCAA 4227
QY 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGlu 551
DB 4228 TATAGCGGA-----AACACCATGGACTCAATCAAGGAGGACTACTA----- 4269
QY 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheThrLeuProAsnAsn 571
DB 4270 TTCACCGTGACACCACTATATCA-----TCAAGTATGAAGCTTGATTCCTGAGAGA 4323
QY 572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTrp----- 582

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Db 4324 AACCTGCTCTAACCAACCAAAATGCCCATTTGGTATGATTATGATACAGACTCTCTG 4383
QY 563 ---HISProGluAspLeuValAspIleIleArgMetGluAspLysGluValIle--- 600
Db 4384 AATAAACCGGATGATCTTAAGCAATATATCTTATGACTGACAGTAAGGAGCTCTACT 4443
QY 601 -----ProValThrHisAsnLeuThrIleu-----ArgLysThrValThr 613
Db 4444 GATGCTCAGGCCCGCTGAGACTTATATCTGCAATTTTCCACGAAAGATTCAGATATA 4503
QY 614 G1LeuAlaG1AspArgThrLysAspPheHisPheGlu----- 626
Db 4504 GTCAAGGCGGGTGGCAGAGCAACTTTTACCGAGATAAAGATGCTCTCCATCAGCA 4563
QY 627 -----1LeG1LeuLysAsnLys 633
Db 4564 TCACCTAGCTTTGATGAATGATATTCATTTAATGCCCTTGAATAGACGGTCTGT 4623
QY 634 G1ng1LeuLeuSerG1nThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652
Db 4624 CTGAATTTTATTAACACTACGCCAGTATGATGTTACTTTTACCAGCATTTGGCAGGAT 4683
QY 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662
Db 4684 GGCCGCAAACTGGGTTATGAAGTTTCAGTATTCCTGTTACCCCTCAGGTAAGTCCGAT 4743
QY 663 GluSerLeuThrLeuG1ng1LeuProGluGlyTyrSerTyrLeuValLysGluThrAsp 682
Db 4744 AATGCCCTGACCTCCACCATATGAAATGATGTCGCGCAATATATG-----CAA 4791
QY 683 SerG1ng1LysValLysValAsnSer-----G1ng1ValAlaAsnLys 698
Db 4792 TGCGAATCTTATGACCCGCTGATATCTATTTGCCCGCCGATGTTGCGAGCGCC 4851
QY 699 ThrValSerLysThrG1yleThrSerAspGluThrLeuAlaPheGluAsnLysGlu 718
Db 4852 ACC-----ACCGAATCGATCAATTCGATGATGAAGAACACAGAAATTCAGGAA 4902
QY 719 ProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIle 738
Db 4903 CCG-----CAGTTAGGCAAAAGTTCTTATGCTACGTTCTGTAT 4941
QY 739 AlaGlyLysLeuGlyLysIleTyrGly 747
Db 4942 CCTCCCTATACCTATCAACTCATGT 4968

RESULT 11
US-08-714-402-1
; Sequence 1, Application US/08714402
; Patent No. 5910441
;
; GENERAL INFORMATION:
; APPLICANT: ROCHA, Claudia
; TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN-BINDING
; TITLE OF INVENTION: PROTEIN FROM GROUP A STREPTOCOCCI
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,402
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

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; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 016921-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-714-402-1

Alignment Scores:
Pred. No.: 1.87e-05 Length: 3531
Score: 150.00 Matches: 192
Percent Similarity: 33.47% Conservative: 127
Best Local Similarity: 20.15% Mismatches: 329
Query Match: 3.80% Indels: 306
DB: 2 Gaps: 50

US-09-494-297-2 (1-757) x US-08-714-402-1 (1-3531)
QY 21 LysAsnSerLysArgPheThrValThrLeuVal-----GlyValPheLeuMetIle--- 37
Db 539 AAACACCGCGGACTGGACAGTGTCTGATGAGAACGGGTATACCAAGTTGGTTGAA 588
QY 38 -----PheAlaLeuValThrSerMetValG1ValAlaLysThrValPheGlyLeuVal 54
Db 569 AATCCCTATATGGGGAATCTACGTAAGCAGGCTCAAAAGATTT----- 636
QY 55 GluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTrp----- 72
Db 637 ---ACTAGTCTTTACAGTTGGAATAATGCCAAATGTCAGTGTCTTAATATATGGAAA 693
QY 73 -----TyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
Db 694 ACAGAGGTAGTAGTGGCGCAGCGGATTTCTACCGCAACCAACGCGCTATTTTAAATG 753
QY 89 Arg-ValAlaIleAsnAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCy 108
Db 754 TCTTTTGAGTTGAACAAACAAAGATTAATCTGAACAAATCAACCCAGGATACCTTTGTG 813
QY 108 sPheAsn-----LeuLys-----LysAlaPhe 115
Db 814 TTACAGCTGATAGACGTCCTCAATCTTAAGGTATCAGTCAAGATATCCCTTAATATAT 873
QY 115 eProLeuGlySerAspSer-----SerValLysLysTrpTyrLysLysHisAspGlyIle 133
Db 874 TACGAC-AGTGCAAATAGTCCGCTTGCGATGGAAATATACATGCTGAGAACCATCAACT 932
QY 133 eSerThrLysPheGluAspTyrAla----- 141
Db 933 TATCTATACTTTCAACAGATTAATATGCGGTTAGATATAAGTCCAGTTGCTCGCAAT 992
QY 142 -----MetSerPr 144
Db 993 GAGCTTATTCCTAGAGATAAGAGAGTGTGGAATACTAGTATCTCAAAATTTTAAGAG 1052
QY 144 CArgG1LeThrGlyAspGluLeuAsnGlnLys-----LeuArgAlaValMetTyrAsnG1 162
Db 1053 TACCATAGTGGCGCAGAGATCACTATTAAGAGAGCGTTATATGTTTATGAAAAGA 1112
QY 162 YHisProGlnAsnAlaAsnGlyIleMetGluGlyLeu-----G1 175
Db 1113 GAGCACTAAAGAAACCAATTAATTAAGATGATGAGCAATGCGGTGGCAGATATGA 1172
QY 175 uProLeuAsnAlaIleArgValThrG1ng1AlaValAlaIlePtyTyrTyrSerAspAsnAlaPr 195
Db 1173 AAGTACAAACACC-----GAAACGGGAGAAATTTGCTGTGATGTTTATGCAATCCAAA 1226

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QY 195 oIleSerAsn---ProAspIleuSerPheIys-----ArgGluSe 207
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 QY 207 rGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnIleuLysGlnLe 227
 Db 1287 TACAAGGCACTTGGAAAAACAGCGTTAATACAGTAGTGTGAGCTGGAGAGATTCCAGGT 1346
 QY 227 uIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp----- 243
 Db 1347 CTATGAAGTACCTGCAAGCAAGAAAAATATACCATCAAGTTATGGGTTATGTTACAAACT 1406
 QY 244 -----PheGlnLeuSerIlePheGln 250
 Db 1407 TACTTTAAGACGATATTCACAGAGCGCTAGCAAAATGTTTCAATATGACCAAAACGTCA 1466
 QY 250 uSerGluAspLysGlyAspLys---TyrAsnLysGlyTyr----- 262
 Db 1467 GCGAATTGACTTTGGAAATATATCCAAATTAAGCATTTATATCATCAAGTACACGGGAA 1526
 QY 263 -----GlnAsnLeuLeuSer----- 267
 Db 1527 AACAGACCAATCTGTATAGCCATTGTTTCAATCCAAATTTGGCAAGTTTCTGTGTC 1586
 QY 268 -----GlyGly----- 269
 Db 1587 TTCTGATATATGCTGCTTTTACTCCAGTTGGAGCAAAATGTCTACTTCCAAACGAATTCG 1646
 QY 270 -LeuValProThrLysProProThrProThrProGlyAspProPheProProAsnGlnProGln 289
 Db 1647 CTGTGCTCCTTCTTAAGGCTAGTGTCTGTGGAAAAAGTAATTT-----ACTAAGCCCTC 1700
 QY 289 nrThrThrSerValLeuLeuLeuArgLysTyrAlaIleGlyAspLysSerLysLeu----- 306
 Db 1701 TATTACAGTACCAATCTAAACAGAGTGGCTCAGCTTCGCTTAAGAAATGTCACTGA 1760
 QY 307 -----LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGln 323
 Db 1761 CAATGTGCCATTTCCAGAACCGCGCTTTTGAGCTGCTCATCAAAATGCTATAGT---CA 1817
 QY 323 nAlaIArgValPheSerSerAsnAspIleGlyGlu-----ArgIleGlnLeuSerAspGln 341
 Db 1818 GAAATTAAGAACCGCATTCACACACACAGAGAGGTTCACTTTAAGAGCCTGACCTGGG 1877
 QY 341 yThrTyrThrLeuThrGlnLeuAsnSerProAlaGlyTyrSer----- 355
 Db 1878 CACATATGACCTGTATGAACAAAGCCCAAAAGGTATACAGAGGTGACAGAGAAATT 1937
 QY 356 -----IleAlaGluProIleThrPhe----- 362
 Db 1938 GGGGACCGTTACTGTGATCTACCAAAACCTGCTGAGGAATGTTGCTACTTGGGGAAGCC 1997
 QY 363 -----LysValGluAlaGlyLysValTyrThrIleLeuAspLysGln-- 377
 Db 1998 ACATTGCTCTGTAAGATGACATACCAAGAGTCAAGTGTCAACATTAAGAAAC 2057
 QY 378 -IleGluAsnProAsnLysGlnIleValGluProTyrSerValGluAlaTyrAsnAspPh 397
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 QY 397 eGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLys 417
 Db 2097 ACCAGAT-----CAACGCCACCAAAAGATTCACATGCAACTGTGTGCA 2138
 QY 417 sAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProProAspSe 437
 Db 2139 AAATGGCTCAA-----AAGTGGCTTAACAGAT 2165
 QY 437 rGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyValLysTyrThrH 457
 Db 2166 TCAGAA-----CTAAGCAAGAT-----AACGATTTGGCTTAT---CA 2201
 QY 457 sIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspTh 477

Db 2202 CTC-----AAAGACTTGGCTAAGTACGATGCCAAAGATCAGAG----- 2241
 QY 477 rPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGluLysGlnAlaI 497
 Db 2242 -----TATAGTATCTCAGTTGAGAAAGTAATGTTCCAGACGGCTACAAAGT 2288
 QY 497 eGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyr 517
 Db 2289 GTCCGTATTTAGAAATGATATATTTAACACACAG-----GAACAGAAATTTGTGTTGACA 2345
 QY 517 rPheThrAspSerAlaGluLeuAspLysAspLysLysAspTyrHisGlyPheGlyAs 537
 Db 2346 GAATTAACCTTAACCTTAATTTGAAATGCTGAATTAAGCAATCTGTGCAAAAT 2405
 QY 537 pMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSer-- 556
 Db 2406 CATGATGAAGACACGCTTAACGCTTTCCAAAGGTAAAGAAATTTGGAAAAATATATACGGC 2465
 QY 557 -----AsnProProGlnIleuThrAspLeuAspPhePhe-----IleProAs 570
 Db 2466 AGAAATCGTCCCAACCATTCACAGTTCAGTTCATGATGAGTGGCTGGAAAG 2525
 QY 570 nAsnAsnLysTyrGlnSerLeuIleGlyThrGlnThrHisProGlu----- 585
 Db 2526 TCAACCAAAATTTATTTCTGCTCAGTGAATGAGTGTGATTTGAAACTTGAA 2585
 QY 586 -----AspLeuVal----- 588
 Db 2586 GAAGTATATGACAGACAGTATATACATATTTCTCAGTTAAAGAACTTAATCTTCCAC 2645
 QY 589 -----AspIleIleArgMetGluAspLysGluVal 599
 Db 2646 AGTTATGATGTACTTACTACAGTATATATATAT-----AATACCAAGCTGAGGT 2699
 QY 599 ILe-----ProValThrHisAsnLeuThrLeuArgLysThrVal 612
 Db 2700 TATTACACAAAGAGACCGAACTAGAGATTGAAGAAACCTTCGCTGACATACAGGTGC 2759
 QY 612 IThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheGlnIleGlu----- 628
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 QY 629 -LeuLysAsnAsnLysGlnIleuLeuSerGlnThrValLysThrAspLys---ThrAs 647
 Db 2814 TTTATACAGTACGACAAAGCTAGTCCGCTGATATGACAAATTGAAGAAAGATGTCTACCA 2873
 QY 647 nLeuGluPheLys-----AspGlyLys-----AlaThrIleAsnLe 659
 Db 2874 TATTAAATTTCTAAACGATGATATTGACGCAAGAGATTAGCTGTGCAACTATGAGT 2933
 QY 659 uLysHisGlyGluSerLeuThrLeuGlnGly----- 669
 Db 2934 GCGGTATTCATCTGTAAACCTATTTAGTACATGATGATTTCAAGTACAGCAAGTAAATTT 2993
 QY 670 -----LeuProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluLysTyr 687
 Db 2994 CTACGCTGATCCAGGAAATATATACATTT---GTGCAAAACCGCAGCAACGAGCTTATGA 3050
 QY 687 sVal-----LysValAsnSerGlnGluValAlaAsnAlaThrValSe 701
 Db 3051 GATAGCAACTGTATTACCTTTACAGTTAATGAGCAA-----GTCACAGTTCTGTAA 3104
 QY 701 rLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValVal 721
 Db 3105 TGGCAAAAGCACTAAAGGTGACACTATATTTGATGCTGATGCTTTACAGCAACTAA 3164
 QY 721 lProThrGly-----ValAspGlnLysIle 729
 Db 3165 GGGTTCAAGTACAGTTATGATATGTAAGAAAGCTT 3201
 RESULT 12
 US-09-327-536-1

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: Sequence 1, Application US/09327536
: Patent No. 6355477
: GENERAL INFORMATION:
: APPLICANT: FISCHETTI, Vincent A.
: TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A
: FILE REFERENCE: 022927-008
: CURRENT APPLICATION NUMBER: US/09/327,536
: CURRENT FILING DATE: 1999-06-08
: PRIOR APPLICATION NUMBER: US 08/714,402
: PRIOR FILING DATE: 1996-09-16
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3698
: TYPE: DNA
: ORGANISM: SFBBP gene
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (196)..(3681)
: US-09-327-536-1

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Alignment Scores:
Pred. No.: 2.02e-05 Length: 3698
Score: 150.00 Matches: 192
Percent Similarity: 33.47% Conservative: 127
Best Local Similarity: 20.15% Mismatches: 329
Query Match: 3.80% Indels: 306
DB: 4 Gaps: 50
US-09-494-297-2 (1-757) x US-09-327-536-1 (1-3698)

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QY 21 LysAsnSerLysArgPheThrValThrLeuVal-----GlyValPheLeuMetIle--- 37
DB 529 AAACACCGCGAGCTTGACAGAGCTGTTATGAGACGGCTATACCAAGTTGGTGA 588
QY 38 -----PheAlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuVal 54
DB 589 AATCCCTAATATGGGGAATCATCATGTAAGCAGGCTCAAAAGATGT----- 636
QY 55 GluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTrp----- 72
DB 637 ---AGTACTTCTTACACTTGGAAATATCCCAAAATGCTGTTTTCNAATATGGA 693
QY 73 -----TyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
DB 694 ACAGAGCTTAGTAGCGCGACGCGATTTCTACCCGACACATGCGCGCTATTTAAATG 753
QY 89 Arg-ValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCy 108
DB 754 TCTTTTGAAGTGAACAAAGATTAATCTGAATCAATCAACCCAGGTATACCTTGTG 813
QY 108 sPheAsn-----LeuLys-----LysAlaPhe 115
DB 814 TTACGCGTGAATAGACGTCTCAATCTTAAGGTATCAAGATATCCCTAAATTCAT 873
QY 115 eProLeuGlySerAspSer-----SerValLysLysTyrTyrLysHisAspGlyI 133
DB 874 TACGAC-AGTCAATATAGTCCGCTGCGATGGAATAATATCATGCTGAGAACATCACT 932
QY 133 eSerThrLysPheGluAspTyrAla----- 141
DB 933 TATCTATACCTTTCACAGATTAATATTGCGGTTTAGATAAAGTCAGTTGCTGCAAAAT 992
QY 142 -----MetSerPr 144
DB 993 GAGCTTATCTCTAGAGATTAAGCAAGTCTGGAAAAATCTAGTATCTCAATTTTAAAG 1052
QY 144 oArgIleThrGlyAspGluLeuAsnGlnLys-----LeuArgAlaValMetTyrAsnG 162
DB 1053 TACATAGTGGCGAGAGATACCTTAAAGAAAGCGTTAATGTCTTTATGAAATGA 1112

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QY 162 yHisProGlnAsnAlaAsnGlyIleMetClnGlyLeu-----G 175
DB 1113 GAGCACTAAAGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1172
QY 175 uProLeuAsnAlaIleArgValThrGlnAlaValIleTyrTyrTyrSerAspAsnAlaPr 195
DB 1173 AAGCTACCAACACC-----GAAGCGGAGAAATTTCTGATGTTATGCAATCCAAA 1226
QY 195 oLleSerAsn---ProAspGluSerPheLys-----ArgGluSe 207
DB 1227 CCGTACCAATATTCCTTATGCGACCATGATTAATTAATTAATTAATTAATTAATTAAT 1286
QY 207 rGluSerAsnLeuValSerThrSerGlnLeuSerIleuMetArgGlnAlaLeuLysGlnLe 227
DB 1287 TACAAGCGACCTTAGAAAACGACGCTAATACAAAGTGTGCTGAGCTTGAGAGATTACAGT 1346
QY 227 uLleAspProAsnLeuAlaThrLysMetProLysGlnValIleProAspAsp----- 243
DB 1347 CTATGAGTACCTGAGAGAGAAAATTTACATCAAGTTATGGGTTGATGTTACAAACT 1406
QY 244 -----PheGlnLeuSerIlePheG 250
DB 1407 TACTTTAAGAACGATATACACAGACGCTTAGAATGTTTCAAAATGACCAACGTC 1466
QY 250 uSerLysAspLysGlyAspLys---TyrAsnLysGlyIle 262
DB 1467 GCGAATTAATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1526
QY 263 -----GlnAsnLeuSer----- 267
DB 1527 AACACACCAATCTGTAAACCATTTGTTTCAATTCATTTTGGCAAGTTTCCGTGTC 1586
QY 268 -----GlyGly----- 269
DB 1587 TTCTGAATATGCTGCTTTTACTCCAGTTGAGAAATGCTACTTCCAAAACGAATTTGC 1646
QY 270 -LeuValProThrLysProProThrProGlyAspProPheMetProProAsnGlnProG 289
DB 1647 CTGTCTCTCTTAAAGGTAGTGTGTTGGGAAAGTGAATTT-----ACTAACCCCTC 1700
QY 289 nThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu----- 306
DB 1701 TATTACAGTAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1760
QY 307 -----LeuGlnGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheG 323
DB 1761 CAATGTGCCATGTCGGAAGCGCGCTTTGAGCTGCTTCATCAATGGAATGATAGT---CA 1817
QY 323 nAlaArgValPheSerSerAspAspIleGlyGlu-----ArgIleGluLeuSerAspG 341
DB 1818 GAATTTAGAACGCTTCAACACACACAGAGAGGTTTACTTTAAAGACCTGACCTCGGG 1877
QY 341 yThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer----- 355
DB 1878 CACATATAGCCTGTATGAACAAAGACCGCAAAAGGTATATCGACGAGTACAGAAAT 1937
QY 356 -----IleAlaGluProIleThrPhe----- 362
DB 1938 GCGCAGCCCTTACTGTTGATACCAACCTGCTGAGGAATAGGCTACCTTGGGAGAGCC 1997
QY 363 -----LysValGluAlaGlyLysValTyrThrIleAspGlyLysGln-- 377
DB 1998 ACATTCGCTGTAAAGTAGAAGCTTAACAAAGAAAGTCAAGATGTCACCATTAAGAAAC 2057
QY 378 -IleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAsp 397
DB 2058 CCTTACGTTTTCAGGGAAGAAATTTGGAG-----AATGACAG 2096
QY 397 eGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsn 417
DB 2097 ACCAGAT-----CAACGCCACCAAGAAATTCAGAGCAACCTGTGCA 2138
QY 417 sAsnGlySerSerGlnValValTyrCyPheAsnAlaAspLeuLysSerProProAspSe 437

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Db      2139 AAATGGTCAA-----AGATGCTTAACAGAT 2165
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Db      2166 TCAAGAA-----GTACGAGAGAT-----AACGATTGGCTTAT---CA 2201
Qy      457 sileAlaGlyARAsPLeuPheLysTyrTrhValLysProARAsPThrAspProAsPth 477
Db      2202 CTTC-----AAGACTGGCTAGTACGATGCCAAGAACATCAGAG----- 2241
Qy      477 rPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgLysLysGlyAlaIle 497
Db      2242 -----TATAGTACTGCTGTAAGAGTAAGTTCAGACGCTCAAGGT 2288
Qy      497 egluTyrSerGlyLeuThrGluTrhGluLeuArgAlaIleThrGluLeuAlaIleTyrTy 517
Db      2289 GTCTATTTAGGAATATATATTATTAACCCAGA--GAACAGAAATTTGTGTTGACA 2345
Qy      517 rPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAs 537
Db      2346 GAATTAACCTTAACCTTGAATTTGGAATGCTGAATAAAGTCAATCTGGTCAAAAAT 2405
Qy      537 pMetAsnAspSerThrIleuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSer-- 556
Db      2406 CATTGATGAAGACACGCTTACGCTTTCAAAGTAAAGTAAGAAATTTGAAATGATACGCG 2465
Qy      557 -----AsnProGluLeuThrAspLeuAspPhePhe-----IleProAs 570
Db      2466 AGAAATTCGTCCTCCACCACTTCAAGTGCAGCTTTATGCTGATGAGTGGCTGTGGAAG 2555
Qy      570 AsnAsnLysTyrGlnSerLeuIleGlyTrhGlnTrhAspProLys----- 585
Db      2526 TCAACCAAAATTTATTTCTGCTCAGTAATGAGTGTCAATTGATTAAAACTTGAA 2585
Qy      586 -----AspLeuVal----- 588
Db      2586 GAAGTATTAATGAACAGTAATGACATCACTTACTCAATTAAGAACTAATCTGCCAAC 2645
Qy      589 -----AspIleIleArgMetGlnAspLysLysGluVal 599
Db      2646 AGGTATGATGTACTTACTCAGCTAATGATATATT-----AATACCAAACTGTAGGT 2699
Qy      599 Iile-----ProValTrhHisAsnLeuThrLeuArgLysTrhVal 612
Db      2700 TATTACACAAAGACAGCAAGCAAGTATGAAAGAAACGCTCCGCTAGATCAGCTGC 2759
Qy      612 IThrGlyLeuAlaGlyAspArgTrhLysAspPheHisPheGluIleGlu----- 628
Db      2760 TTCAAGC-----GGTACCACTACTGTGCAAGACTCAGCCCAAGTATACCTTATCAGG 2813
Qy      629 -LeuLysAsnAsnLysGlnLysLeuLeuSerGlnTrhValLysThrAspLys--ThrAs 647
Db      2814 TTTATCAAGTACGACCAAGTACGTCGGTATGACATTAATGAAGAAATAGTGTACCCA 2873
Qy      647 nLeuGluPheLys-----AspGlyLys-----AlaThrIleAsnLe 659
Db      2874 TATTAAATTTCTCAAAAGCTGATATGTCGCAAGAGTATAGTGTCACTATAGAGTT 2933
Qy      659 uLysHisGlyGluSerLeuThrLeuGlnGly----- 669
Db      2934 GCGTGATTCATCTGGTAAACATATTATGATCATGATTCAGATGACAACTGAAGAATTT 2993
Qy      670 -----LeuProGluGlyTyrSerTyrLeuValLysGluTrhAspSerGluGlyTyrTy 687
Db      2994 CTACCTGATGCCAGAAATATATACATT---GTGCAAAACCGCAGCACACGCTTATGA 3050
Qy      687 sVal-----LysValAsnSerGlnLysValAlaAsnAlaThrValSe 701
Db      3051 GATAGCAACTGTATTACTTTACAGTTAATGAGCAA-----GGTCAGGTTACTGTAAA 3104
Qy      701 rLysTrhGlyIleThrSerAspGluTrhLeuAlaPheGluAsnAsnLysGluProValIva 721

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Db      3105 TGGCAAGCACTAAAGGTGACACTATATTGTCATGGTTGACAGCCAACTAA 3164
Qy      721 lProThrGly-----ValAspGlnLysIle 729
Db      3165 GCGTTCAGGTACAGTTATGATATATGAAAGAAACGTT 3201

RESULT 13
US-08-447-031A-8
: Sequence 8, Application US/08447031A
: Patent No. 5851794
:
: GENERAL INFORMATION:
:   APPLICANT: GUS, Bengt
:   APPLICANT: HOOK, Magnus
:   APPLICANT: JONSSON, Hans
:   APPLICANT: LINDBERG, Martin
:   APPLICANT: PATRI, Joseph
:   APPLICANT: SIGNAS, Christer
:   TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
:   TITLE OF INVENTION: ITS PREPARATION
:   NUMBER OF SEQUENCES: 8
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Burns, Doane, Swecker & Mathis
:     STREET: P.O. Box 1404
:     CITY: Alexandria
:     STATE: Virginia
:     COUNTRY: United States
:     ZIP: 22313-1404
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/08/447, 031A
:     FILING DATE: 22-MAY-1995
:     CLASSIFICATION: 435
:     PRIOR APPLICATION DATA:
:       APPLICATION NUMBER: US 07/861,804
:       FILING DATE: 21-AUG-1992
:       PRIOR APPLICATION DATA:
:         APPLICATION NUMBER: WO PCT/SE91/00707
:         FILING DATE: 22-OCT-1991
:         APPLICATION NUMBER: SE 9003374-7
:         FILING DATE: 22-OCT-1990
:         ATTORNEY/AGENT INFORMATION:
:           NAME: McGowan, Malcolm K.
:           REGISTRATION NUMBER: 39,300
:           REFERENCE/DOCKET NUMBER: 012889-006
:           TELECOMMUNICATION INFORMATION:
:             TELEPHONE: (703) 836-6620
:             TELEFAX: (703) 836-2021
:             INFORMATION FOR SEQ ID NO: 8:
:               SEQUENCE CHARACTERISTICS:
:                 LENGTH: 4612 base pairs
:                 TYPE: nucleic acid
:                 STRANDEDNESS: single
:                 TOPOLOGY: linear
:               MOLECULE TYPE: DNA (genomic)
:               FEATURE:
:                 NAME/KEY: CDS
:                 LOCATION: 931..4485
:
: US-08-447-031A-8
:
: Alignment Scores:
:   Pred. No.: 3.7e-05
:   Score: 149.00
:   Percent Similarity: 34.11%
:   Best Local Similarity: 19.25%
:   Query Match: 3.78%
:   DB: 2
:   Gaps: 41

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US-09-494-297-2 (1-757) x US-08-447-031A-8 (1-4612)

[illegible]

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QY	414	-----AlatylsAsnlyAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeu	431
Db	2689	GACATTACCGAAGTATGATGAAGGA---AAGAAATAGAAATATACAGTGCACGGAAGATCAC	2745
QY	432	LysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPheThrGly	451
Db	2746	GTAAGAAGACTACACACAGACATCACGCTGACGACAAATACGAAACAAAGTATACACAGGA	2805
QY	452	GluValLysTyrThrHisIlelaGlyLysrAsp-----	462
Db	2806	GAGCATGTGGCACAACAGTAAACAAAAATTGGCATGCAATTAATACCAAGACGGAACACA	2865
QY	463	-----LeuPhe-----LysTyrThrValLysProArgAsp	472
Db	2866	CCAACTGAAATCAAAAGTGGATTATATACAGCGGAAAGCAAGCAAGCAAGCAAGCAAGCA	2925
QY	473	ThrAspProAspThrPheLeuLysHisIleLysLysValIleGlyLysGlyTyrArgGlu	492
Db	2926	TTAAATGAATCTAATTAAGTGCACCCATACGTGACAGCAAGATTATGATGA---AAACCA	2979
QY	493	LysGlnAlaIleGlyLysSerGlyLeuThrGlnThrGlnLeuArgAlaAlaThrGln	512
Db	2980	AAAGGACAAACAAAGTAAATATACACAGTACGAGAAATTAACAAAGGTCAAGTTATACACA	3039
QY	513	-----IleuAlaIleTyrTyrPheThrAspSer	521
Db	3040	CATGTGATTAACATATATATGGTAACTGATGTCAGCAATTAATTAATCCACCAACAAA	3099
QY	522	AlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSer	541
Db	3100	ACATCAATTTAGTGGGAAAAAAGTATAGGAC-----GACAAAGACAAAT---	3144
QY	542	ThrIleuAlaValAlaLysIleLeuValGlyTyrAlaGlnAspSerAsnProProGlnLeu	561
Db	3142	-----CAAGATGTGTAAAGACACCAAGAAAA	3165
QY	562	ThrAspLeuAspPhePheIleProAsnAsnLysTyrGlnInsLeu-----Ile	578
Db	3166	GTCAGTGTGAAT---TTATGTGGCTGATGAGAGAAAGTAAAAACGTTAGACGTGACATCT	3222
QY	579	GlyThrGlnTyrHisPheGluAspLeuValAspIleIleArgMetGluAspLysLysGlu	598
Db	3223	GAAACAAATGGAAGTACAGAA---TTTAAAGACTTACCGAAGTATGATGAAGGAAGAA	3279
QY	599	ValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaLysAsp	618
Db	3280	ATA-----GAAATACACAGTGACCC-----GAAAGAT	3303
QY	619	ArgThrLysAspPheHisPheGluIle-----	627
Db	3304	CACGTAAAGACTACACACAGACATCAAGCTGACGACAAATTAACGACAAAGATATACACA	3366
QY	628	-----GluLeuLysAsnAsnLysGlnGluLeu	636
Db	3364	GGAGAGCATGGCGCAACAGTAAACAAAAATTGGCATGCAATTAATTAACCAAGACGGA	3422
QY	637	LeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspGlyLys-----	654
Db	3424	CGAACCACTGAATTAAGAGTTGAGTTA-----TATCAAGACGCAAAACCAACA	3471
QY	655	-----AlaThrIleAsnLeuLysHisGlyLysSerLeuThrLeuGlnGlyLeu---	670
Db	3472	GGAAAGACGCAACATTAATGAAATCTAATTAAGCTGACCCATACCTGACAGAGATTATAT	3533
QY	671	-----ProGluGlyTyrSerTyrLeuValLysGlu---ThrAspSerGlyGly	685
Db	3532	GAAAAAGCAAAACCAACCACTAAATTAATTAACAGTCCAGCAATTAACAAAGGTCAAGGT	3591


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Db 4402 ACAGCCTATTATTAATAACACAGCCAGTCCCATTTGAAATTCGTAGAGAAAATGCTGGT 4461
Oy Lys-----ValThrIle 372
Db 4462 AAACACGGGCTGCTGCTGCTAGTACAACTTTGTGACTTTACAAAGGGCTTTCCAAATC 4521
Oy 373 IleAspGlyLysGlnIleGluAsnPro----- 381
Db 4522 GTGAAACAGAAATAGCGCAGACCAACCATTTAGCAGTGTCTTTTGAATTAATATGATCAC 4581
Oy 382 AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSer 401
Db 4582 AATAAACA-ATCATTAGGATATACAG- AAGCAGTGGCAAGATGAG-- 4625
Oy 402 ValLeuThrThrGlnAsnTyr-----AlaLysPhe-TyrTyrAlaLysAs 416
Db 4626 -----CAAAATATCTTTTAGAGACTTGGCGCAGGTACTTATTAATACAAAGA 4673
Oy 416 n-----LysAsnGlySerSerGlnValValTyrCys----- 426
Db 4674 AATCAACAGCACCAAAATTAACGATGGCGCAGATTAATTAATTCCTGCAATTAGTAAA 4733
Oy 427 -----PheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThr 444
Db 4734 AGTAGAAATTCGTGCTGATTCATCAAGGTGATCCGAGATT----- 4773
Oy 444 tThrProAspPheThrThrGlyGluValLysTyrThrHisIleAlaGlyArgAspLeu 464
Db 4774 -----TTCCAAATAGGG-----GCCCTGCCCAATTCAAAGGCGGCGCTCT 4817
Oy 464 eLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLys 484
Db 4818 TAGAGAAATTCATGTCGCAATGCGAACCCACTTCCAGAAAGATTTAAATTTATGCA-- 4875
Oy 484 sValIleGluLysGlyTyrArg-----GluLysGlyGlnAl 496
Db 4876 -----ATCGAAACGGGCAAAAATCTTTGAAGAGAAAGTAACGTGCTGCAAGATGCTTC 4931
Oy 496 aIle-----GluTyrSerGlyLeuThrGluThrG 506
Db 4932 ATTGCTATGAGAGATTAGTGTGCTGCTAGCTATGATTAATGATGAATGATGATGATGATG 4991
Oy 506 nLeuArgAlaIleThrGlnLeuAlaIleTyrThrPhe-----ThrAsp 521
Db 4992 TGGCTATATCGCATTAACAACCCATTTATTTTGTAGTGAAGAATTCAAATGATTA 5051
Oy 521 tAlaGluLeuAspLysAspLysLeuLysAspTyrHisGly-----PheGly----- 536
Db 5052 ACAACCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5111
Oy 537 -AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp 556
Db 5112 CAACGAGCAAGGTCAACCTTAGCGGTGCACTTTTGCATTTCAATTCAAATTCGCGATGACA 5171
Oy 556 tAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGln 576
Db 5172 GAATAGGCCCAAGGTTACCGATATCATTTCTTGAAATGCTGACGAGAAAGAAAGTTTTCGA 5231
Oy 576 t----- 576
Db 5232 AATAACACGATAGACTGGGAAATTTACGCTAAAGGGCTAATGAAGGCATTAGCT 5291
Oy 577 -----LeuIleGlyThrGlnTyrHisProGluAs 586
Db 5292 TTTAGTGAACGAAAGACACCAACAGGCTATCTTGAACACACAGCTACATCA- 5346
Oy 586 PheValAspIleIleArgMetGluAspLysLysGluValIleProValThrHisAsn 606
Db 5347 -----TTTGATGTAACCGCCCAATTAGGAAAGACAGCAATTCGTTTAGGCGATCTAT 5402
Oy 606 uThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheG 626
Db 5403 CAATATATCAAGAACTGCT-----CA 5423

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Oy 626 uIleGluLeuLysAsnAsnLysGlnIleLeuLeuSerGlnThrVal-----LysThrAs 644
Db 5424 ATTAAACAAAGAAAGAAACGAAACGATGCAAGCATTTGCGAGTGTGCTTTAAGTATGTA 5483
Oy 644 PLSYThrAsnLeuGluPheLysAspGlyLysAlaThrIle-----AsnLeuLysHisGly 663
Db 5484 TGAACACAGG---CAACCGTAGATGAGCAACCAATCTGATGCTGACAAACGACGCA 5540
Oy 663 uSerLeuThrLeuGlnGlyLeuProGluGlyTyr----- 674
Db 5541 AGTCATTCGCAAAAACCTTAGCACCGGAAACGATGCTTTTGTGAGACACAAGCCCAAC 5600
Oy 675 -SerTyrLeuValLysGluThrAspSerGluLysTyrLys----- 687
Db 5601 TAGCTATCTCTTAATGAAGACGCAAGCGCAAGCTTTACGATTTGCCAAAGACCAAG 5660
Oy 687 ----- 687
Db 5661 CAACCCAGCAGCTGCTGCTAATTAAGCAACCTTTATTAATTAACCAAGTGTGCCAAGCT 5720
Oy 688 -ValLysValAsnSerGlnGluValAlaAsnAla----- 698
Db 5721 GGTGAATAATGATCAGCAAAAGATGCCCTTACAGAGTCTCAATTTAAAGTGACAGATGC 5780
Oy 699 -----ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheG 714
Db 5781 AGACAGCGGCAACATTCGCTGCTCATTTACGTTCTGACAAACGAGGTAGTTCAAGT 5840
Oy 714 uAsnAsnLysGluProValAlaProThrGlyValAspGlnLysIle-----AsnGlyTyr 732
Db 5841 GAACCACTTACACACGAAATATACCTTTTGTGAACAAAGACCGGATGCTTAC 5898

RESULT 15
US-09-071-035-461
; Sequence 461, Application US/09071035
; Patent No. 6448043
;
; GENERAL INFORMATION:
; APPLICANT: GILL H. CHOI
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; FILING DATE:
; TELEPHONE: (301) 309-8512
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 461:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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US-09-071-035-461

Alignment Scores:

Score:	5.94e-05	Length:	6168
Percent Similarity:	149.00	Matches:	181
Best Local Similarity:	32.02%	Conservative:	120
Query Match:	19.26%	Mismatches:	320
	3.78%	Indels:	320
		Caps:	45

US-09-494-297-2 (1-757) x US-09-071-035-461 (1-6168)

QY 19 LeuSerLysAsnSerLysArgPheThValThrLeuValGlyValPheLeuMetIlePhe 38
 Db 3361 CTGAGAAACAGACGCTGATGAGACGACTATTTTACGAGCGCCCTTCCAAATTTGG 3420
 QY 39 AlaLeuValThrSerMetVal-----GlyAlaLysThr 49
 Db 3421 GACCAAGCTAAACACACAGTCTACGTGAAGGTACAGTACGACCGGCGTTATGCACA 3480
 QY 50 ValPheGly-----LeuValGlySerSerThrProAsnAlaIle 62
 Db 3481 TTGTGTGGTTCGCCACAAAGGCAATACATTTTGTGGAGACAAAGACCA----- 3531
 QY 63 AsnProAspSerSerSerGluTyrArgTrpTyrGlyTyrGluSerTyrValArgGlyHis 82
 Db 3532 -----GAGGCTATACAGTTTCGGAC 3552
 QY 83 ProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArg 102
 Db 3553 GAATTAGCTAAAGGCCAGTCATCTACTATTGATGAGAAACTTACGCCGAAGGACACAA 3612
 QY 103 SerTyrGlnValTyrCysPheAsnLeuLysAlaPheProLeuGluGlySerAspSerSer 122
 Db 3613 CCA---ACCATTTTAAACAGATGTCATTAAGTATTTTAAAGAAAATGATGAGAGAAG 3669
 QY 123 ValLysLysTrp-----TyrLysLysHisAspGlyIleSerThrLysPhe--- 137
 Db 3670 GGTAAGAAAGTTAGTCATCTCGCTGCTTAAATTTAGAGCATCCGCTACACGCGCTTTACT 3729
 QY 138 -----GluAspTyrAlaMetSerProArgIleThrGlyLysAspGluLeuAsnGlnLysLeu 155
 Db 3730 CATTTGGAGAAAGTTCCTCCCTTGGCGCGATCGAAC----- 3765
 QY 156 ArgAlaValMetTyrAsnGlnLysProGlnAsnAlaAsnGlyIleMetGlu-----Gly 173
 Db 3766 -----AACGCCAATGGCCAGTTAGAGGTGATAGT 3795
 QY 174 LeuGluPro---LeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAsp 192
 Db 3796 TTAAACCCAGGCTTTATCATGTTCCAGAAATCGAACACCGACCGCTATCTTTTAGAC 3855
 QY 193 AsnAlaPro----- 195
 Db 3856 ACAGACCCCAACAGATTCAATCGTGACCAAAATACGACGCGCAAAATTCGTATGTTCAAT 3915
 QY 196 -----IleSerAsnProAspGluSerPheLysArgGluSerGluSerAsn 210
 Db 3916 GTCAAAATGCTTAATTACCAAGGTTCGTCGAACATAATTAAGAAAGCAACAGCGCAAT 3975
 QY 211 LeuValSerThrSerGlnLeuSerLeuMet-----ArgGlnAlaLeuLysGln--- 226
 Db 3976 CCATTTAGCGAGTCTGTAATTTTCAAGTCTTGACACACAGACAGACAGATTTGCGAACAC 4035
 QY 227 ---LeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln 245
 Db 4036 TTAGTTTCGATCGAAACCGAAAAAGTCACAGTACGATTTAGCCCGACGAAAAATATACAA 4095
 QY 246 LeuSerIlePheGluSerGluAspLysGlyAspLysTrpLysGlyTyrGlnAsnLeu 265
 Db 4096 TTT-----GIGAAACCAAGGCCCA----- 4116
 QY 266 LeuSerGlyLysLeuValProThrLysProProThrProGlyAspProPromeProPro 285

Db 4117 ---GCAGGCTACCTTTTAAACACTGAACCAAGTGTTCACGATTCGACGACGATCGG 4173
 QY 286 AsnGlnProGlnThr-----ThrSerVal 293
 Db 4174 GGCAAACCCAAACAGTATTATGACAGCGGCTAACTTTGTTACATCATCAGACGCGCTAAA 4233
 QY 294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluAlaThrLeuGln 313
 Db 4234 TTATATCAAAAGATGTGATGCA-----CACTATTATAGTGTGCGACATTTAA 4284
 QY 314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGly 333
 Db 4285 GTGCTTGATCGAAGGAGAGAAAGATTCAAACAGCGCTTG---ACGACAAATATATCAAGG 4341
 QY 334 GluArgGly-----GluLeuSerAspGlyTyrThrThrLeuThrGluLeuAsnSerPro 351
 Db 4342 GAATTTGTCACAGACCTTAGCCGCCAGAAATATCGCTTTGTAGAAACCAAGCGCCA 4401
 QY 352 AlaGlyTyrSerIle---AlaGluProIleThrPheLysVal-----GluAlaGly 367
 Db 4402 ACAGGCTATTATTAAATACACGCGCAGTCCATTGGAATTCGTGAGAAAAATGCTGGT 4461
 QY 368 Lys-----ValTyrThrIle 372
 Db 4462 AAACACGCGTGTGCTGTAGTACAACTTTGTGATTAACAAGGCGCTTCCAAATC 4521
 QY 373 IleAspGlyLysGlnIleGluAsnPro----- 381
 Db 4522 GTGAAAACGAATATGCGGACGACCAACCTTTAGCAGGCTCTTTTTCGAATATATGATCAC 4581
 QY 382 AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSer 401
 Db 4582 AATAAACA-AATCATTTAGGATTTACAGC-----AACGATGGCAAAATGCG--- 4625
 QY 402 ValLeuThrThrGlnAsnTyr-----AlaLysPhe-TyrTyrAlaLysAs 416
 Db 4626 -----CAAAATTTCTTTAGAGACTTGGCGCCGAGTACCTATTATTATTAACAAGA 4673
 QY 416 n-----LysAsnGlySerSerGlnValValTyrCys----- 426
 Db 4674 AATCAAAAGCACCAAAATTTACCAATGCGCGAGATTAATATTATTTATTCGAAATTAAGTAAA 4733
 QY 427 -----PheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
 Db 4734 AGTAGAAATTCGTGATGATTTCAAAAGGTATCCGAGATTT----- 4773
 QY 444 tThrProAspPheThrThrGlyValValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
 Db 4774 -----TTCCAATTTAGG-----GCCTTCGCCAATTTCAAGAGACGCGCGCTTT 4817
 QY 464 eLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisLysLeu 484
 Db 4818 TAAGAAATTTGATGCCAATCGAACCCACTTCCAGAGACGATTTTAAATTTGATATGCA-- 4875
 QY 484 sValIleGluLysGlyTyrArg-----GluLysGlyGlnAl 496
 Db 4876 ---ATCGAAACCGGGAAGAAATCTTTGAAGAAGAAGTAATCGTGAAGAAACATGCTTC 4931
 QY 496 aIle-----GluTyrSerGlyLeuThrGluThrG 506
 Db 4932 ATTGGCTATGAGAGATTTAGTGTGCTGTAGCTATGAAATTTAGATGAACGTGATCAACGCA 4991
 QY 506 nLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe-----ThrAspSe 521
 Db 4992 TGCGCTATATCGCAATTAACACCATTTATTTTGTAGTGAGAGAAAGAAATTCAAATATTA 5051
 QY 521 rAlaGluLeuAspLysAspLysLeuLysAspTyrHisGly-----PheGly----- 536
 Db 5052 ACAACCACTAGATGAGTTAGAGTTGTAATTTATCAAGCAAGAAATATGAGAGCTAAAGT 5111
 QY 537 -AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSe 556
 Db 537 ----- 556


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Db 5112 CAACGACGAAGTCAAACTTAGCGGGTGCAGTTTTCATTTACATGCCGATGACA 5171
QY 556 rAsnProGlnLeuThrAspLeuAspPheIleProAsnAsnLysIleGlnSe 576
Db 5172 GAATCAGCCCCCAAGTTACCGATACATCTTGAAATCGTCAGAGAAAAAGTTCTGA 5231
QY 576 r----- 576
Db 5232 AATTACACGATTAAGCTGGCGCAATTACGCTAAAGGCTAAATGAGGCAATTACGT 5291
QY 577 -----LeuIleGlyThrGlnTrpHisProGluAs 586
Db 5292 TTATGTGAAGCAAGAACGACCAACAGGCTATCTGTAGACACACAGCTACATCCA----- 5346
QY 586 pLeuValAspIleIleArgMetGluAspLysLysGluValIleProValThrHisAsnLe 606
Db 5347 ----TTTGATGTAAACCCCGCCCAATTAGGAAAGACAGCCAAATGCTTTAGCGCATCTTAT 5402
QY 606 uThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheG1 626
Db 5403 CAATTATCAAGAACTGCT-----CA 5423
QY 626 uIleGlnLeuLysAsnLysGlnGlnLeuLeuSerGlnThrVal-----LysThrAs 644
Db 5424 ATTAAACCAAGAAAGCAAGACAGGTGAAGCATTTGCAAGTGGGTGTTAAGTCATTGA 5483
QY 644 pLysThrAsnLeuGlnPheLysAspGlyLysAlaThrIle--AsnLeuLysHisGlyG1 663
Db 5484 TGAACACAGGG--CAAAACCGTAGTGACAAACCAATCTGATGTGACAAAGCAAGCAA 5540
QY 663 uSerLeuThrLeuGlnGlnLeuProGluGlyTyr----- 674
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QY 675 -SerTyrLeuValLysGlnThrAspSerGluGlyTyrLys----- 687
Db 5601 TAGCTATCTTCTTATATGAACGCCAAGCGCATGCTTACGATGCCAAAGACACCAAG 5660
QY 687 ----- 687
Db 5661 CAACACGACCTGTGTACTTAAGCACCTTTTATTATTAATTAACCAAGTGCTGCCAAGCT 5720
QY 688 -ValLysValAsnSerGlnGlnValAlaAsnAla----- 698
Db 5721 GGTAAAAATGTATCAGCAAAAGAAATGCTTAGCAGGTGCTGAATTTAAAGTACAGATGC 5780
QY 699 -----ThrValSerLysThrGlyIleThrSerAspGlnThrLeuAlaPheG1 714
Db 5781 AGAGACAGGCAAACTGTCGTGATTAAGCTTGACACCAAGGTTAGTTCAAGT 5840
QY 714 uAsnAsnLysGlnProValValProThrGlyValAspGlnLysIle--AsnGlyTyr 732
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Search completed: August 19, 2003, 18:23:10
Job time : 211 secs

